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Figure 1.1

Recombinant bifunctional single-chain protein

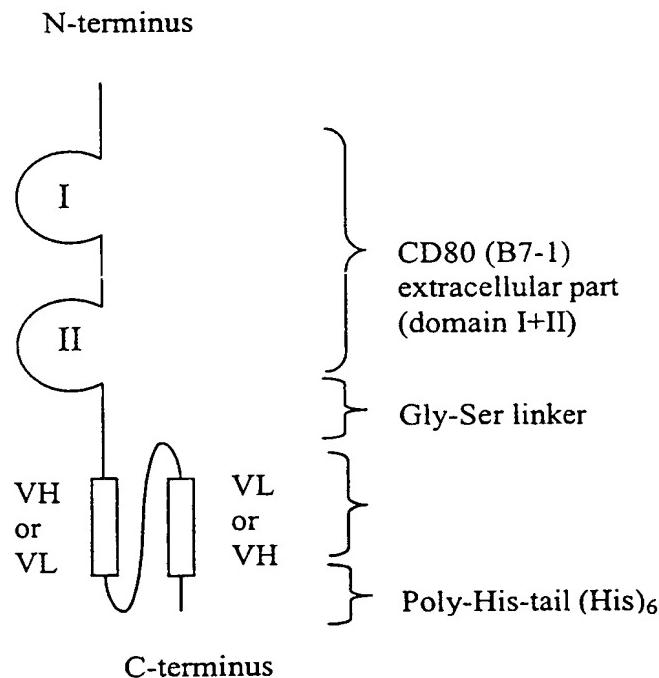


Figure 1.2 DNA-sequence designated CTI

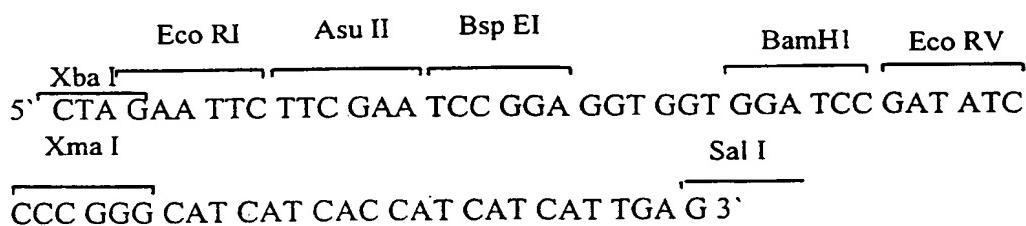


Figure 1.3 Design of various bifunctional CD80-scFv-constructs

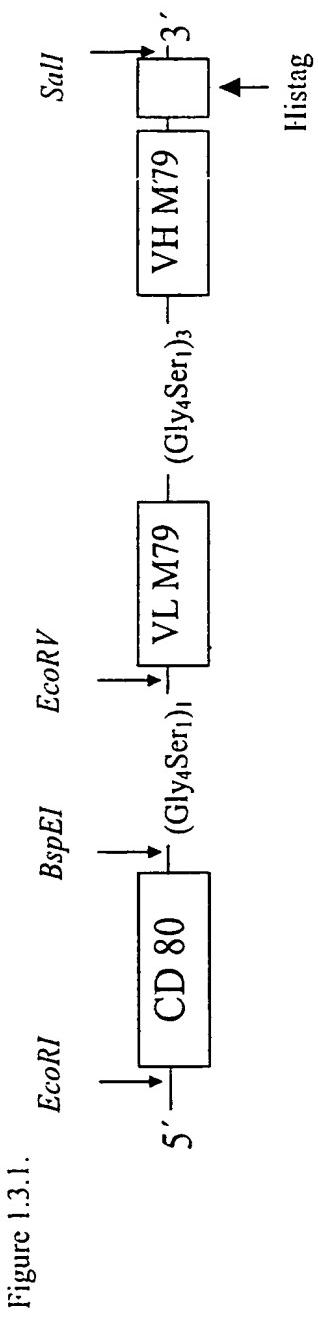


Figure 1.3.2.

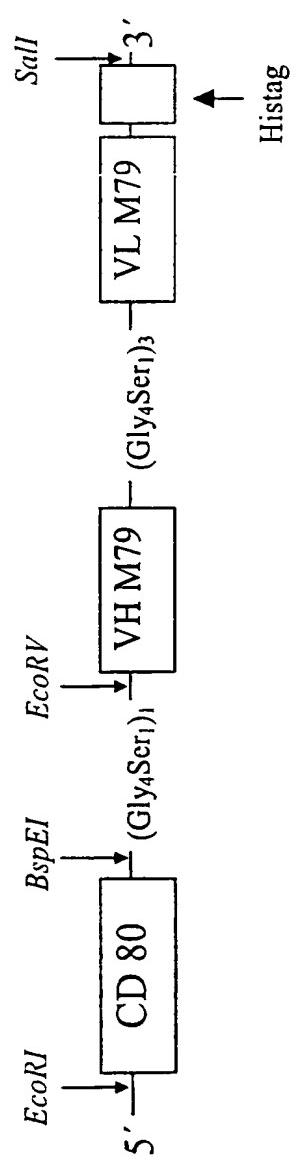


Figure 1.3.3.

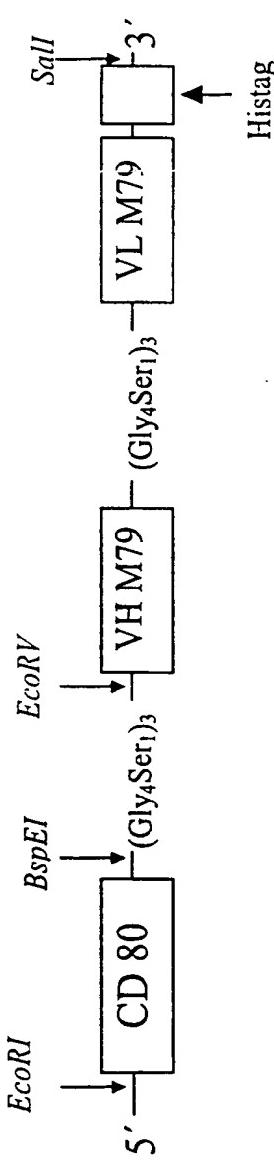


Figure 1.3.4.

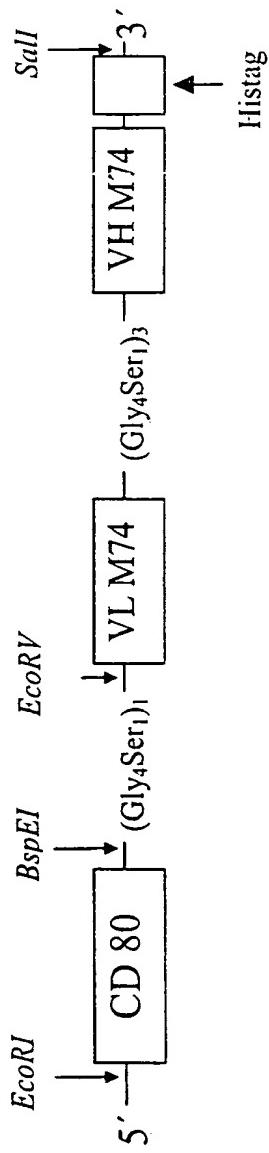


Figure 1.3.5.

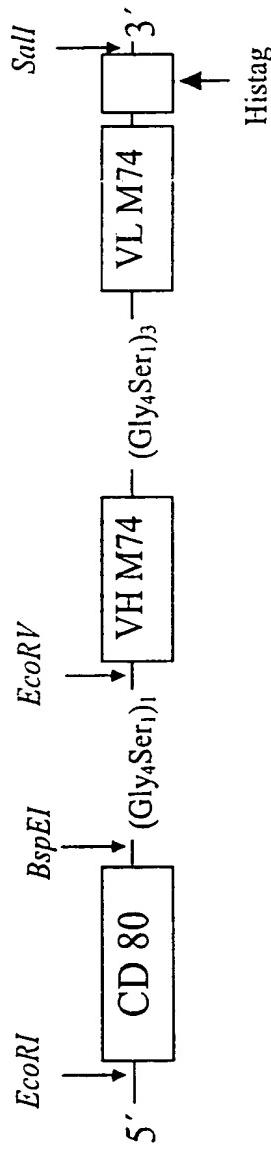


Figure 1.3.6.

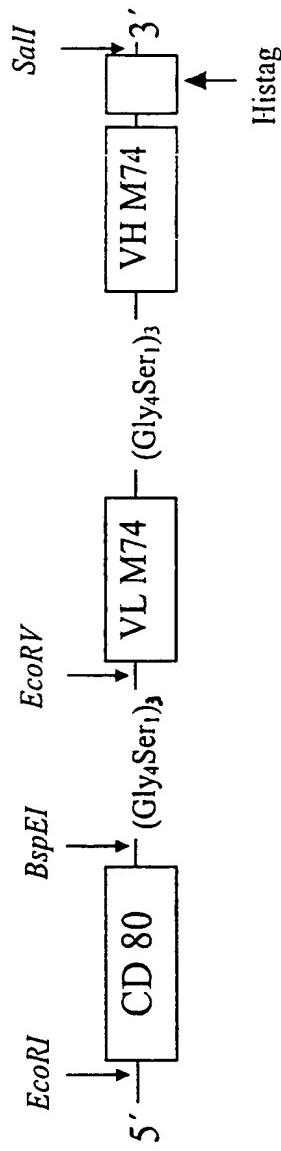


Figure 1.3.7

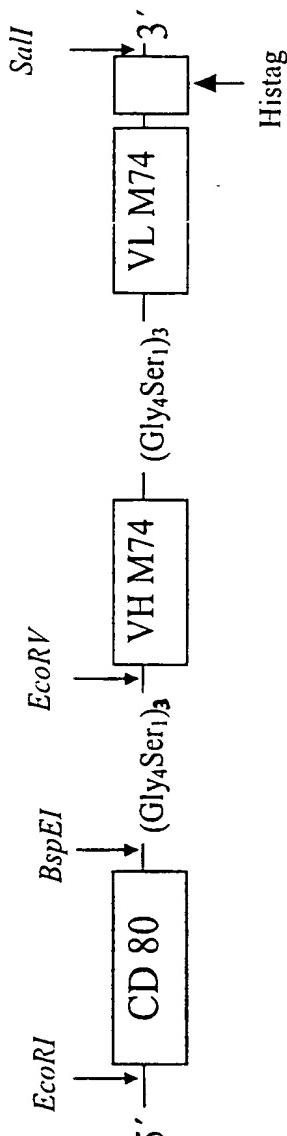


Figure 1.3.8.

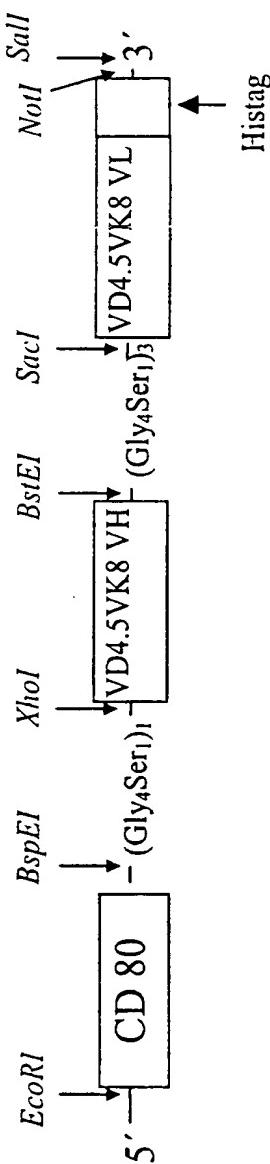


Figure 1.3.9.

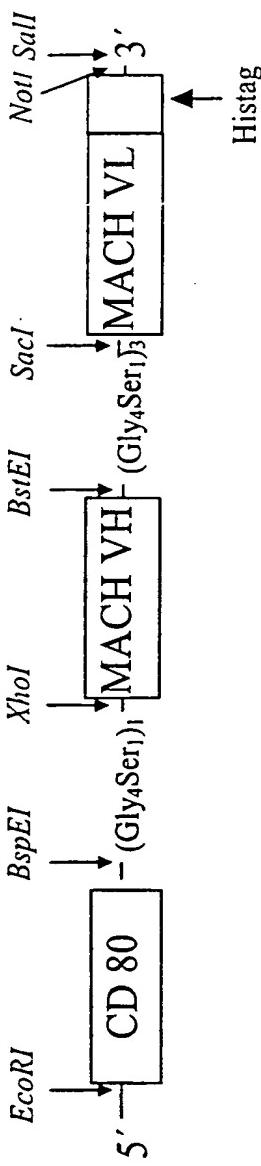


Figure 1.4

ELISA-analysis
CD80-M79scFv (VL/VH) with short linker
Detection: anti-His-tag

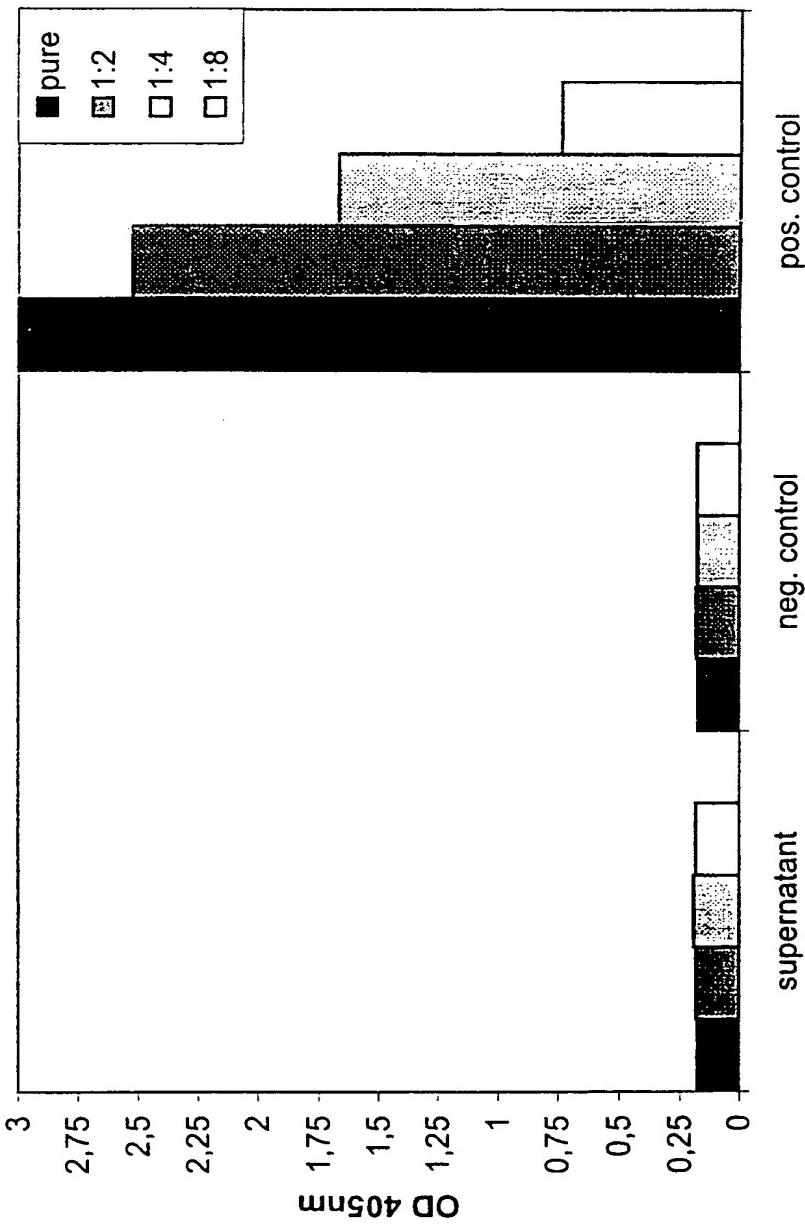


Figure 1.5

ELISA-analysis
CD80-M79scFv (VL/VH) with short linker
Detection: anti-CD80

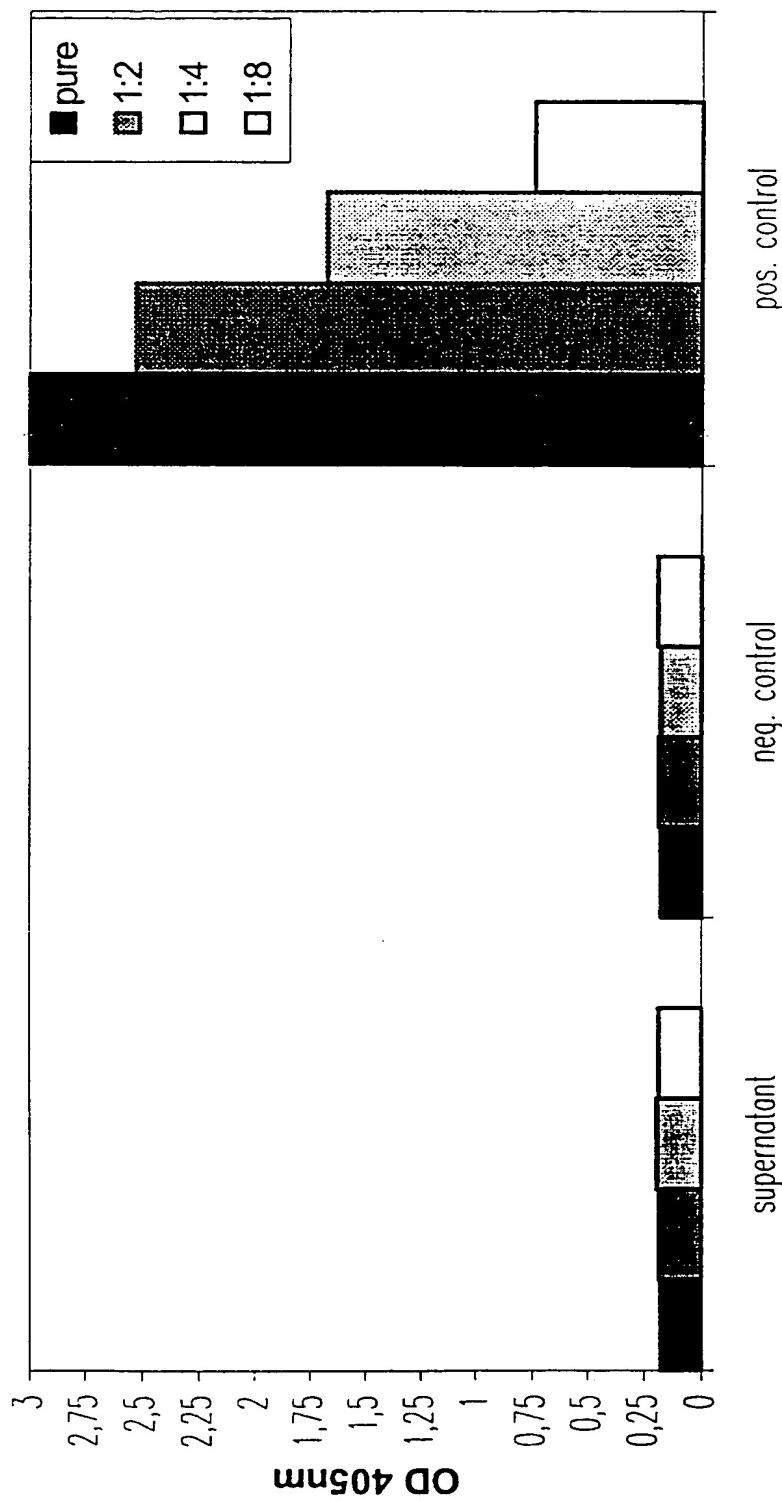


Figure 1.6

ELISA-analysis
CD80-M79scFv (VL/VH) with short linker
Detection: anti-His-tag or anti-CD80 (as indicated)

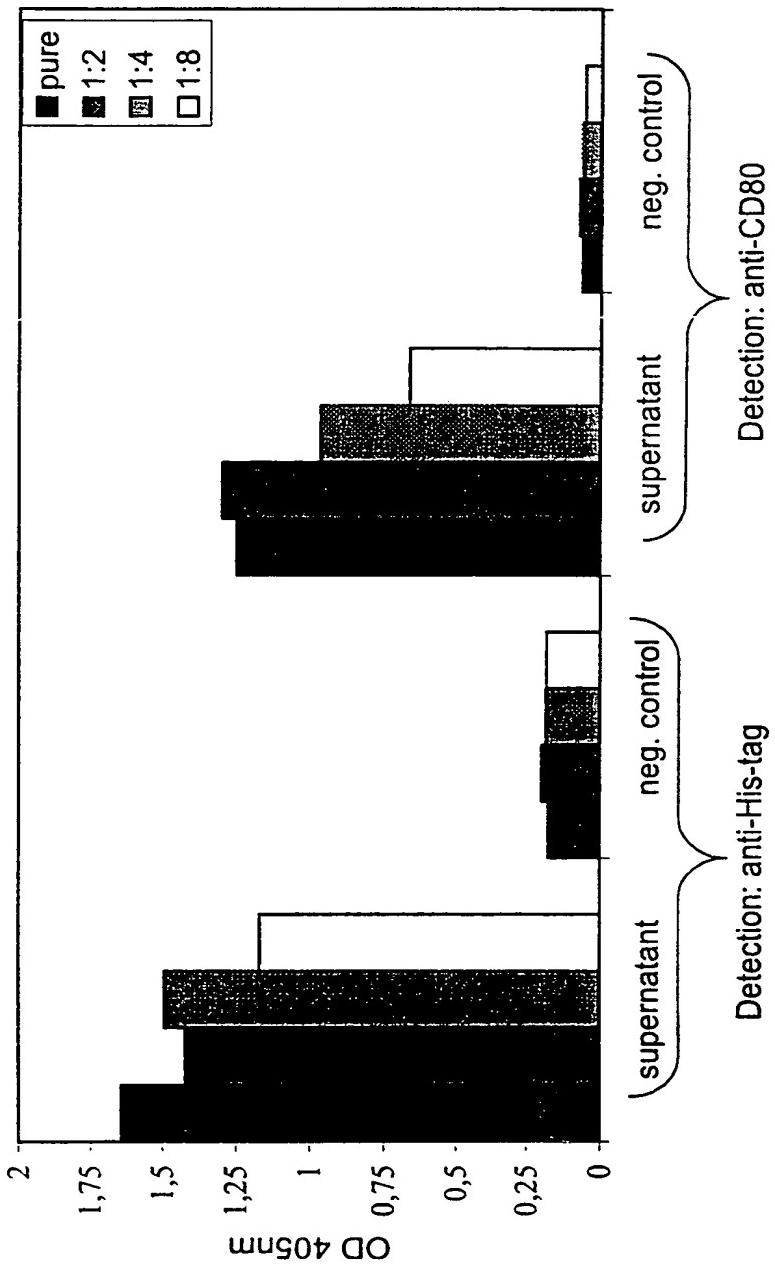


Figure 1.7

ELISA-analysis
CD 80-M 79 scFv (VH/VL) with short linker
Detection: anti-CD 80

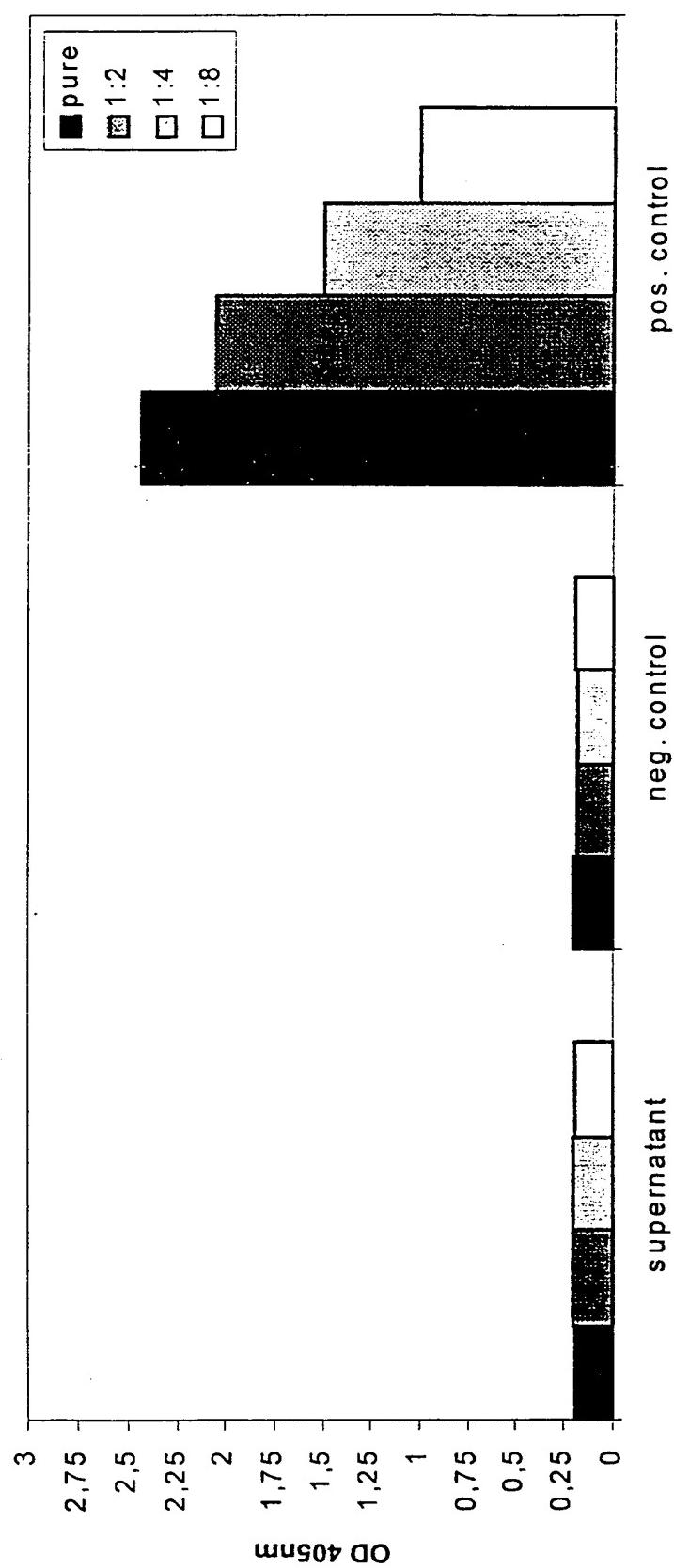


Figure 1.8 DNA-sequence of double-stranded oligonucleotide designated ACCGS15BAM

BspE1 Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly
 5' pCC GGA GGT TCC GGG GGT TCA GGT GGT GGT G 3'
 3' T CCA CCA AGG CCC CCA CCT CCA AGT CCG CCA CCA CCTAG 5'

Figure 1.9

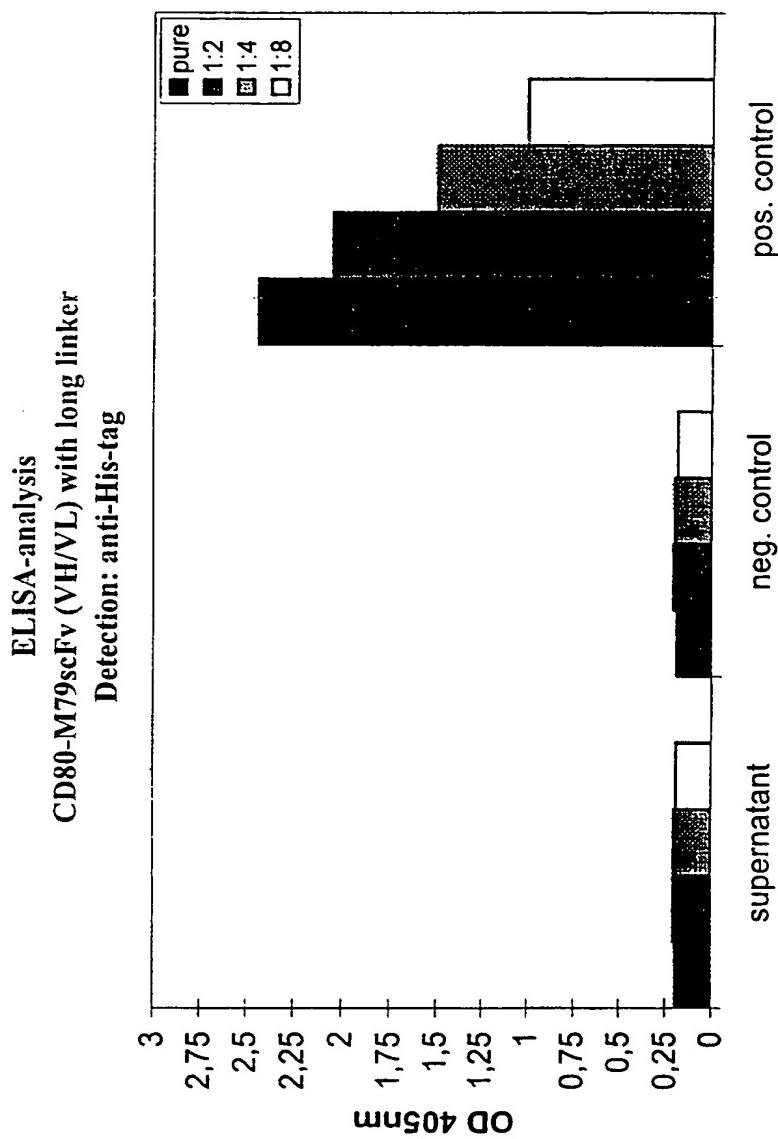


Figure 2.1

Elisa-analysis
CD80-M74 scFv with different linker lengths and either
VL/VH- or VH/VL-domain arrangement (as indicated)
Detection: anti-His-tag

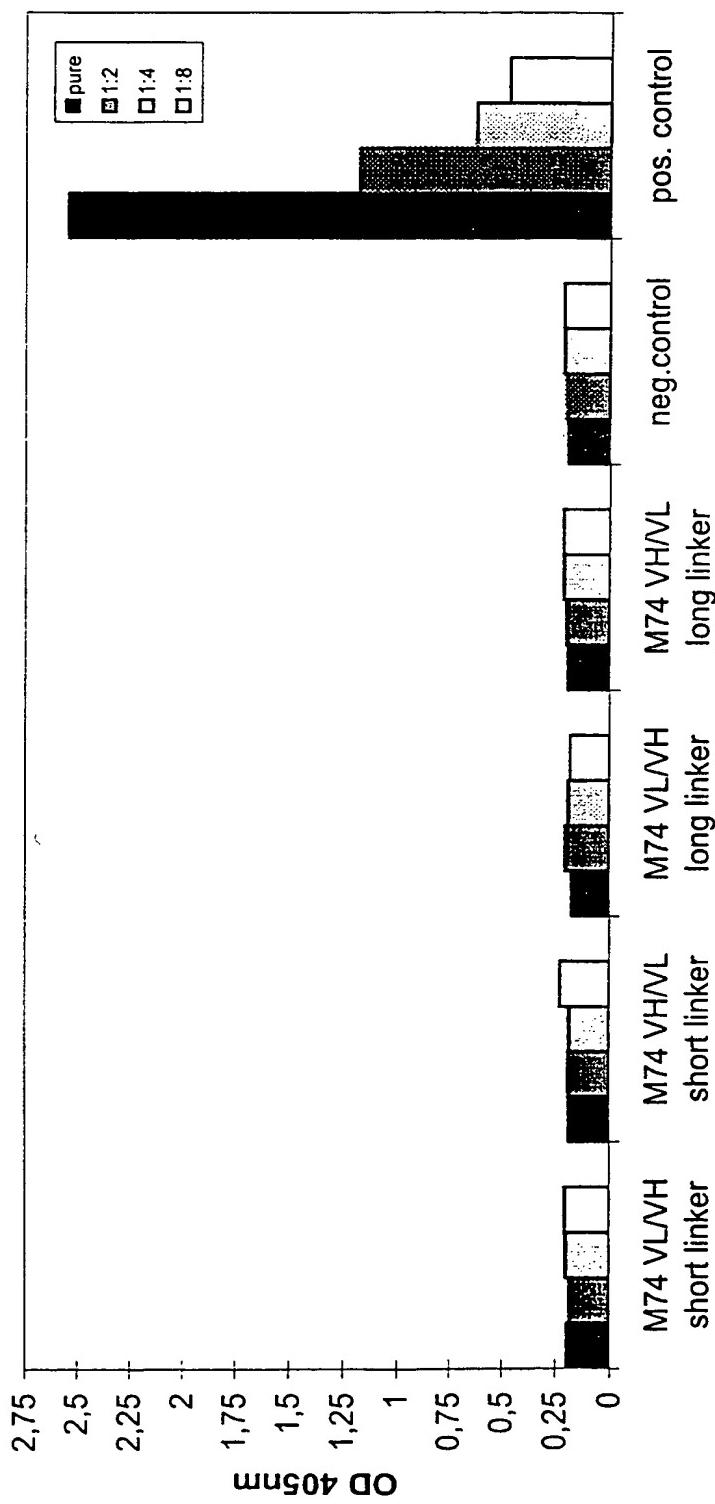


Figure 2.2

ELISA-analysis
CD80-M74 scFv with different linker lengths and either
VL/VH- or VH/VL-domain arrangement (as indicated)
Detection: anti-CD80

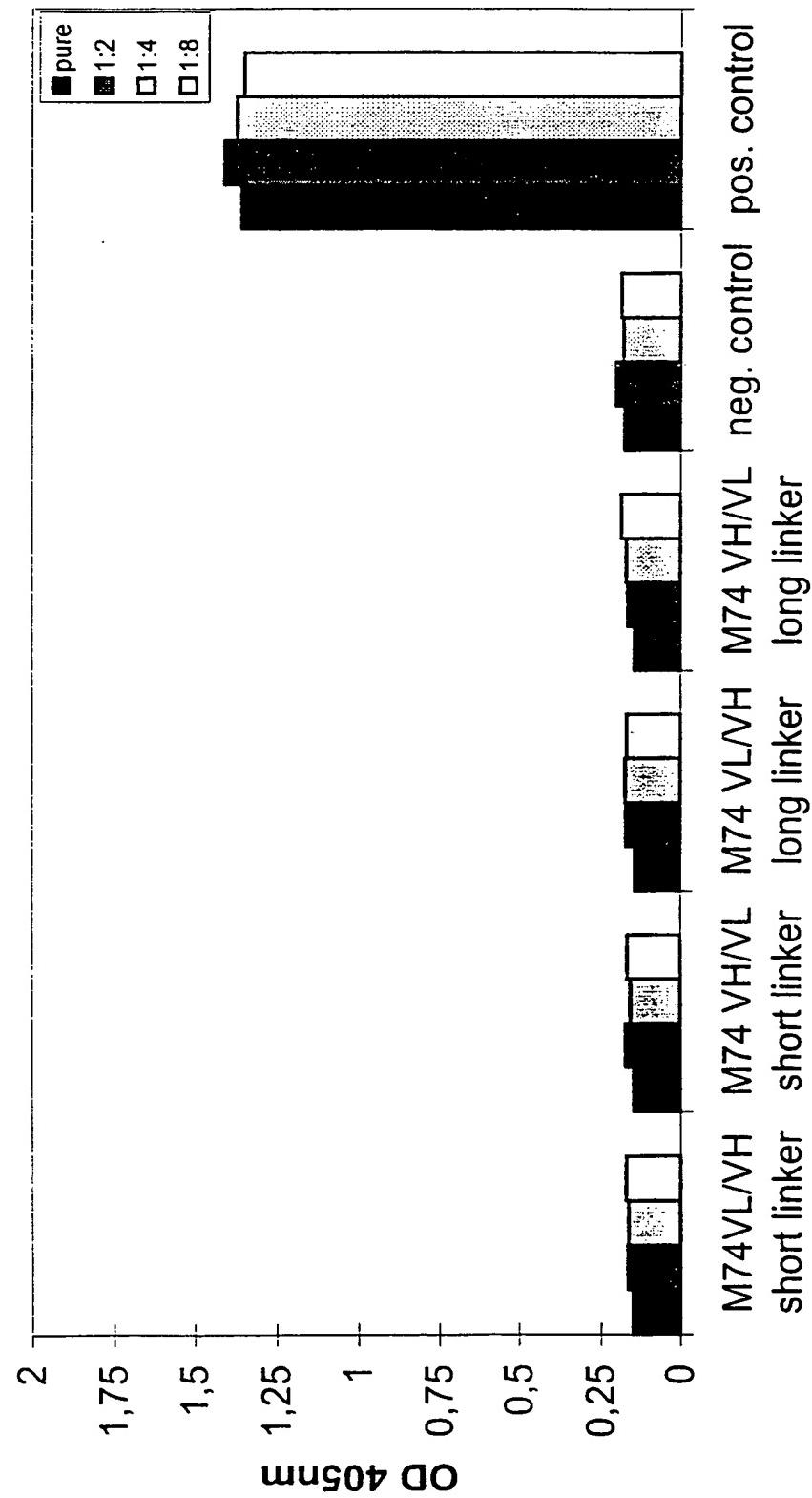


Figure 3.1

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5'	GAG	GTG	CAG	CTG	CTC	GAG	TCT	GGG	GGA	GGC	GTG	GTC	CAG	CCT	GGG	AGG	TCC	CTG
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	E	V	Q	L	L	E	S	G	G	G	V	V	Q	P	G	R	S	L
	63					72			81			90			99			108
	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTC	AGT	AGC	TAT	GGC	ATG	CAC	TGG
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	R	L	S	C	A	A	S	G	F	T	F	S	S	Y	G	M	H	W
	117					126			135			144			153			162
	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	GCA	GTT	ATA	TCA	TAT	GAT
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	V	R	Q	A	P	G	K	G	L	E	W	V	A	V	I	S	Y	D
	171					180			189			198			207			216
	GGA	AGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	CTG	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	G	S	N	K	Y	Y	A	D	S	V	K	G	R	F	T	I	S	R
	225					234			243			252			261			270
	GAC	AAT	TCC	AAG	AAC	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D
	279					288			297			306			315			324
	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AAA	GAT	ATG	GGG	TGG	GGC	AGT	GGC	TGG	AGA	CCC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	T	A	V	Y	Y	C	A	K	D	M	G	W	G	S	G	W	R	P
	333					342			351			360			369			378
	TAC	TAC	TAC	GGT	ATG	GAC	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	Y	Y	Y	Y	G	M	D	V	W	G	Q	G	T	T	V	T	V	S

TCA 3'

S

Figure 3.2

14/40

	9	18	27	36	45	54
5'	GAG CTC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCT TCT GTG GGA GAC AGA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	E L Q M T Q S P S S L S A S V G D R					
	63	72	81	90	99	108
	GTC ACC ATC ACT TGT CGG ACA AGT CAG AGC ATT AGC AGC TAT TTA AAT TGG TAT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	V T I T C R T S Q S I S S Y L N W Y					
	117	126	135	144	153	162
	CAG CAG AAA CCA GGA CAG CCT CCT AAG CTG CTC ATT TAC TGG GCA TCT ACC CGG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	Q Q K P G Q P P K L L I Y W A S T R					
	171	180	189	198	207	216
	GAA TCC GGG GTC CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	E S G V P D R F S G S G S G T D F T					
	225	234	243	252	261	270
	CTC ACC ATC AGC AGT CTA CAA CCT GAA GAT TCT GCA ACT TAC TAC TGT CAG CAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	L T I S S L Q P E D S A T Y Y C Q Q					
	279	288	297	306	315	
	AGT TAC GAC ATC CCG TAC ACT TTT GGC CAG GGG ACC AAG CTG GAG ATC AAA 3'					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	S Y D I P Y T F G Q G T K L E I K					

Figure 3.3

**ELISA-analysis
soluble VD4.5VK8-scFv-fragment
Detection: anti-His-tag**

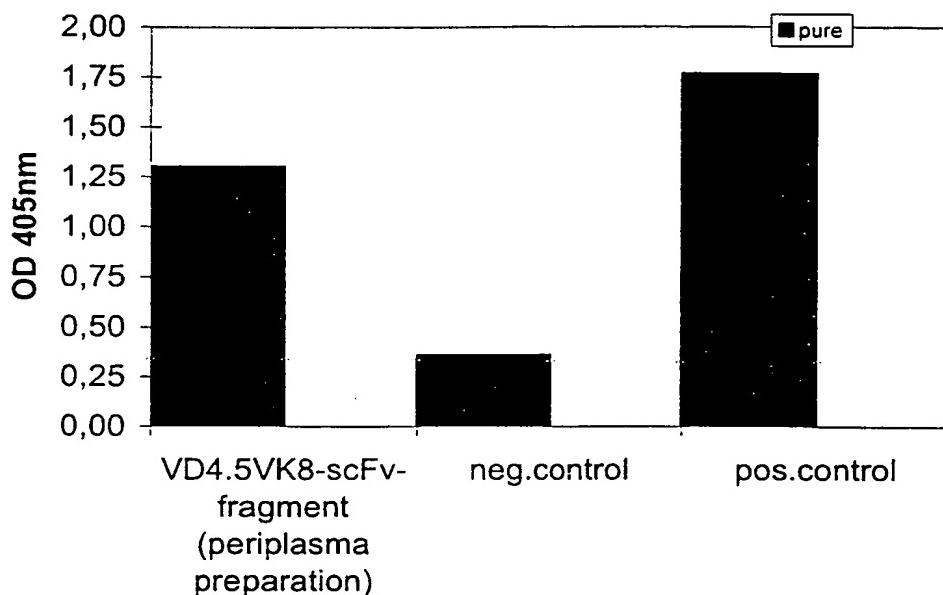


Figure 3.4 DNA-sequence designated L-F-NS3Frame

Figure 4

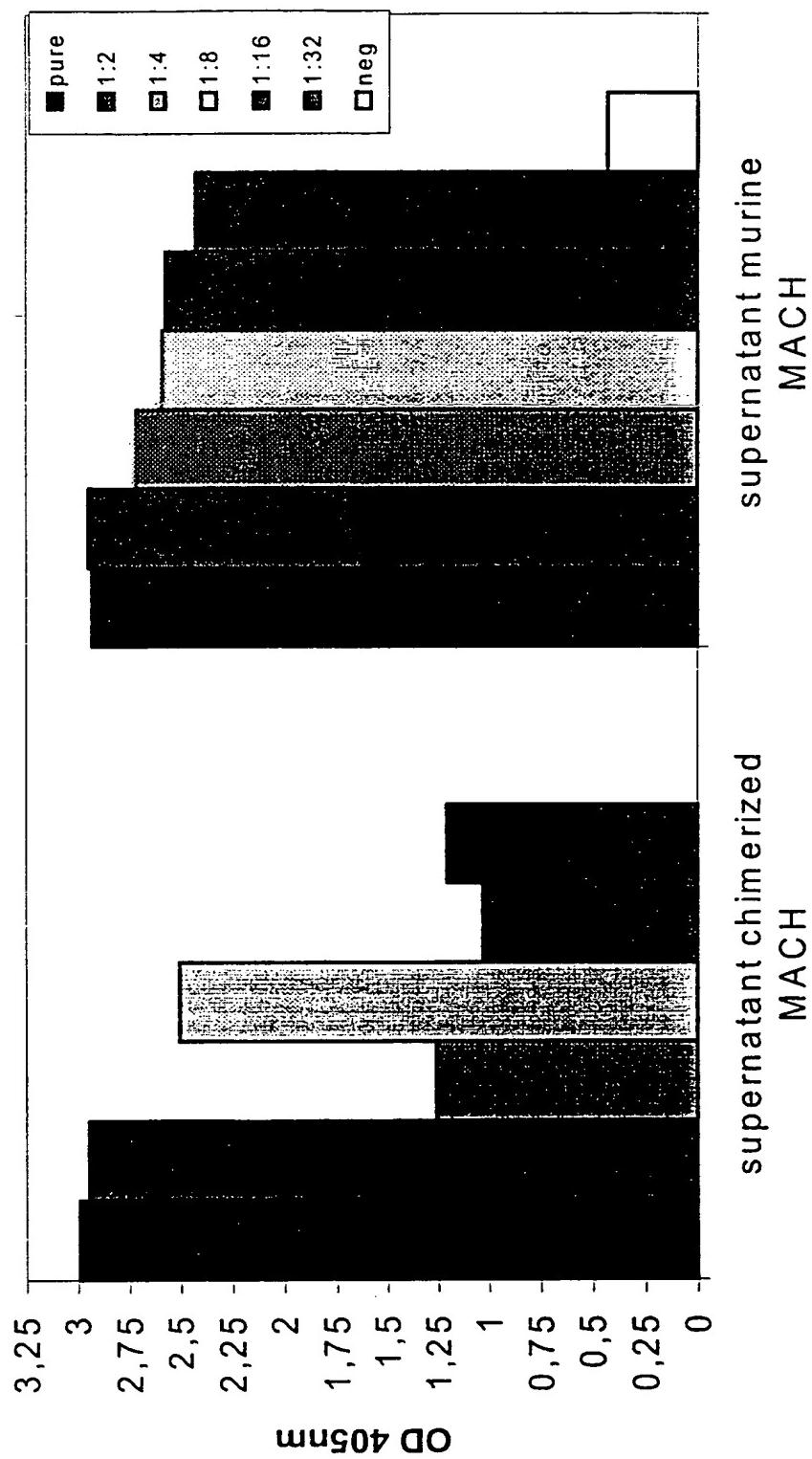
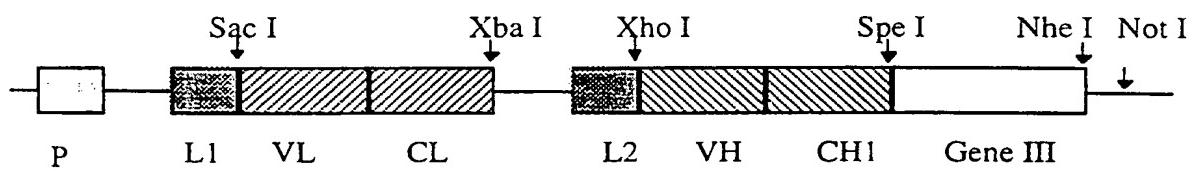


Figure 5.1

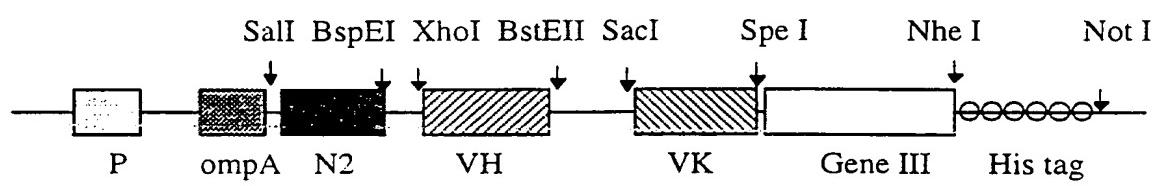


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Figure 5.2

destroyed

Figure 5.3



DRAFT - NOT FOR FILING

Figure 6.1

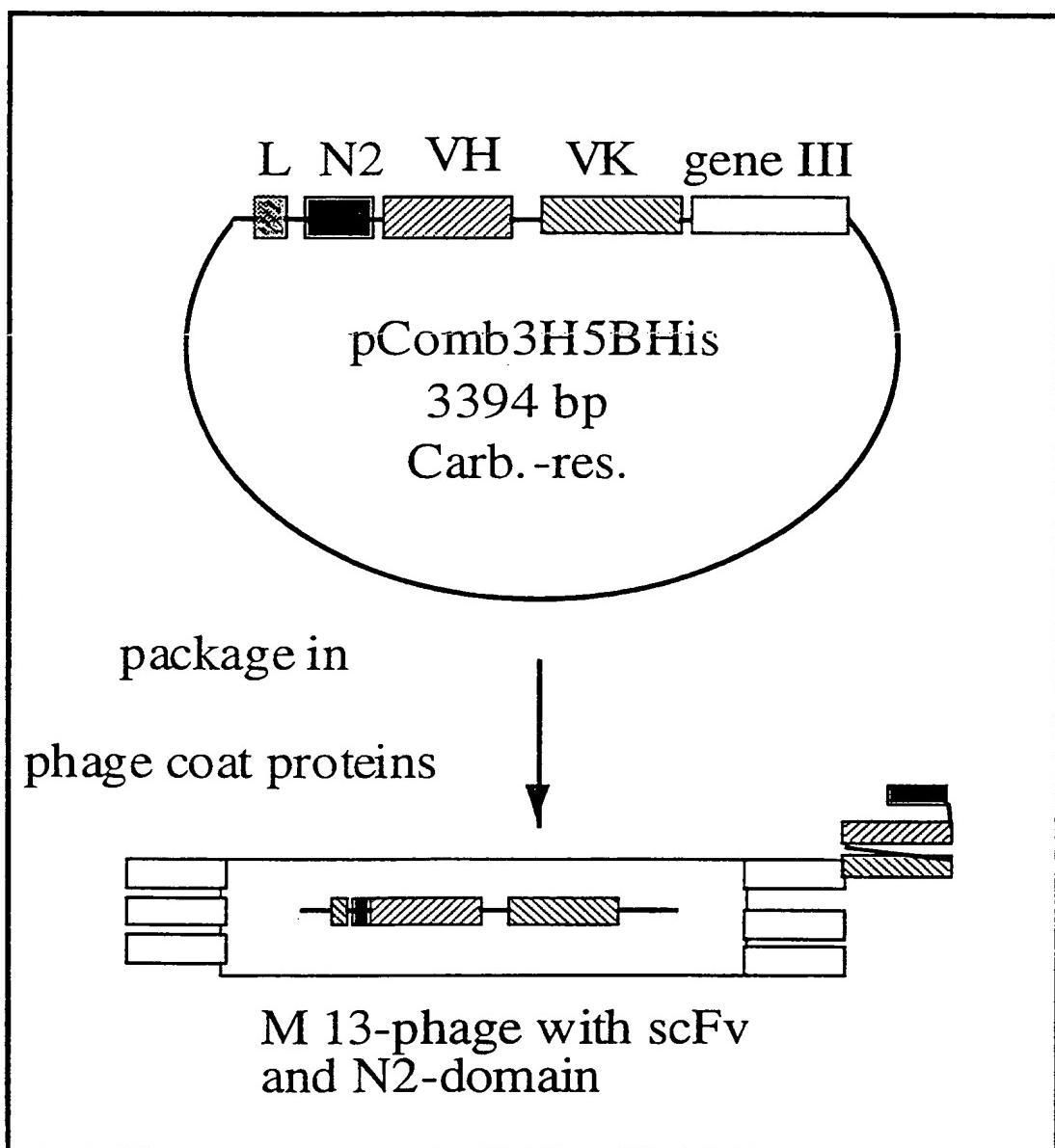


Figure 6.2

PANNING ASSAY FOR CLONALITY

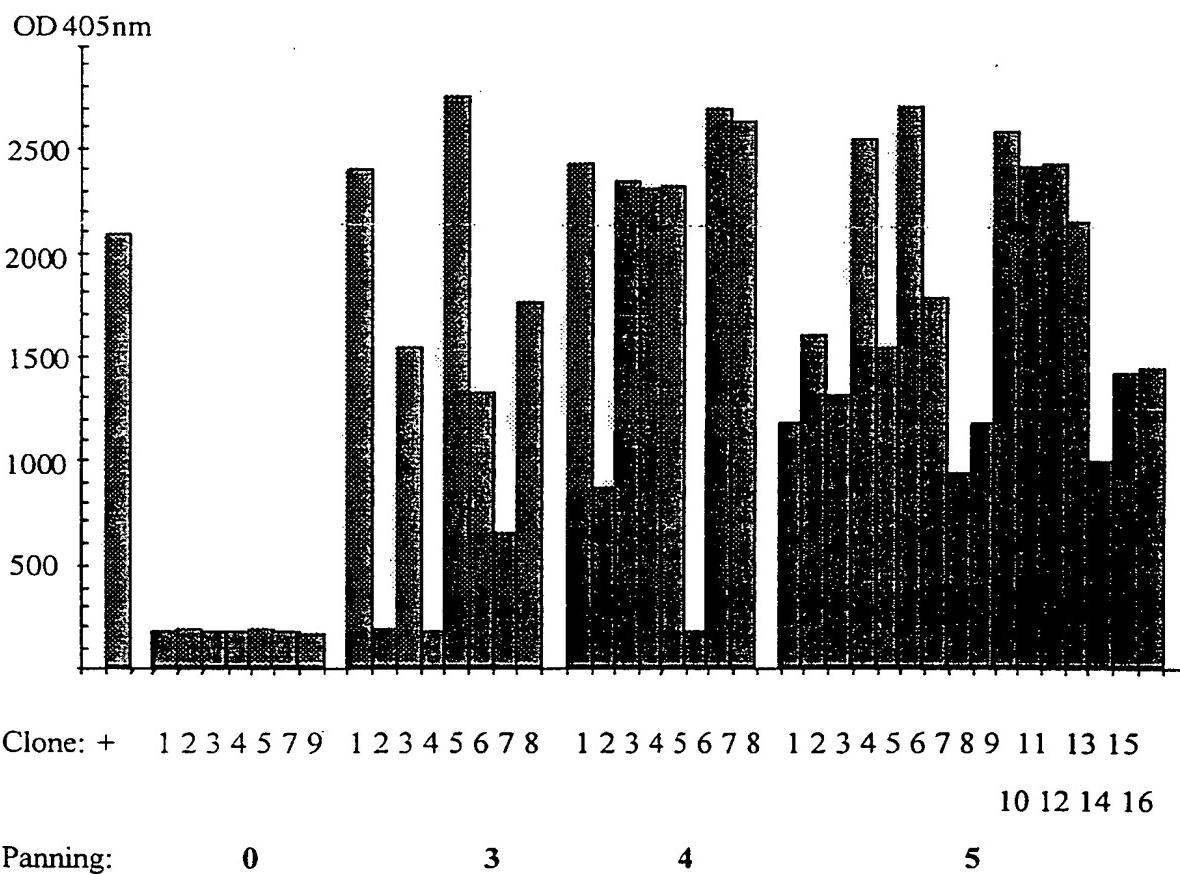


Figure 6.3

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	9	18	27	36	45	54
5	GAG GTG CAG CTG CTC GAG CAG TCT GGA GCT GAG CTG GTG AAA CCT GGG GCC TCA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	E V Q L L E Q S G A E L V K P G A S					
	63 72 81 90 99 108					
	GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC GCC TTC ACT AAC TAC TGG CTA GGT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	V K I S C K A S G Y A F T N Y W L G					
	117 126 135 144 153 162					
	TGG GTA AAG CAG AGG CCT GGA CAT GGA CTT GAG TGG ATT CGA GAT CTT TTC CCT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	W V K Q R P G H G L E W I G D L F P					
	171 180 189 198 207 216					
	GGA AGT GGT AAT ACT CAC TAC AAT GAG AGG TTC AGG GGC AAA GCC ACA CTG ACT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G S G N T H Y N E R F R G K A T L T					
	225 234 243 252 261 270					
	GCA GAC AAA TCC TCG AGC ACA GCC TTT ATG CAG CTC AGT AGC CTG ACA TCT GAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	A D K S S S T A F M Q L S S L T S E					
	279 288 297 306 315 324					
	GAC TCT GCT GTC TAT TTC TGT GCA AGA TTG AGG AAC TGG GAC GAG GCT ATG GAC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	D S A V Y F C A R L R N W D E A M D					
	333 342 351 360 369 378					
	TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GGT GGT GGT TCT GGC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	Y W G Q G T T V T V S S G G G G S G					
	387 396 405 414 423 432					
	GGC GGC GGC TCC GGT GGT GGT TCT GAG CTC GTC ATG ACC CAG TCT CCA TCT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G G G S G G G S E L V M T Q S P S					
	441 450 459 468 477 486					
	TAT CTT GCT GCA TCT CCT GGA GAA ACC ATT ACT ATT AAT TGC AGG GCA AGT AAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	Y L A A S P G E T I T I N C R A S K					
	495 504 513 522 531 540					
	AGC ATT AGC AAA TAT TTA GCC TGG TAT CAA GAG AAA CCT GGG AAA ACT AAT AAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	S I S K Y L A W Y Q E K P G K T N K					
	549 558 567 576 585 594					
	CTT CTT ATC TAC TCT GGA TCC ACT TTG CAA TCT GGA ATT CCA TCA AGG TTC AGT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	L L I Y S G S T L Q S G I P S R F S					
	603 612 621 630 639 648					
	GGC AGT GGA TCT GGT ACA GAT TTC ACT CTC ACC ATC AGT AGC CTG GAG CCT GAA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G S G S G T D F T L T I S S L E P E					
	657 666 675 684 693 702					
	GAT TTT GCA ATG TAT TAC TGT CAA CAG CAT AAT GAA TAT CCG TAC ACG TTC GGA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	D F A M Y Y C Q Q H N E Y P Y T F G					
	711 720					
	GGG GGG ACC AAG CTT GAG ATC AAA 3'					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G G T K L E I K					

Figure 6.4

23/40

	9	18	27	36	45	54												
5.	GAG	GTG	CAG	CTG	CTC	GAG	CAG	TCT	GGA	GCT	GAG	CTG	GTA	AGG	CCT	GGG	ACT	TCA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	E	V	Q	L	L	E	Q	S	G	A	E	L	V	R	P	G	T	S
	63					72			81			90			99			108
	GTG	AAG	CTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	ACA	AGC	TAT	GGT	TTA	AGC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	V	K	L	S	C	K	A	S	G	Y	T	F	T	S	Y	G	L	S
	117					126			135			144			153			162
	TGG	GTG	AAG	CAG	AGA	ACT	GGA	CAG	GGC	CTT	GAG	TGG	ATT	GGA	GAG	GTT	TAT	CCT
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	W	V	K	Q	R	T	G	Q	G	L	E	W	I	G	E	V	Y	P
	171					180			189			198			207			216
	AGA	ATT	GGT	AAT	GCT	TAC	TAC	AAT	GAG	AAG	TTC	AAG	GGC	AAG	GCC	ACA	CTG	ACT
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	R	I	G	N	A	Y	Y	N	E	K	F	K	G	K	A	T	L	T
	225					234			243			252			261			270
	GCA	GAC	AAA	TCC	TCC	AGC	ACA	GGC	TCC	ATG	GAG	CTC	CGC	AGC	CTG	ACA	TCT	GAG
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	A	D	K	S	S	S	T	A	S	M	E	L	R	S	L	T	S	E
	279					288			297			306			315			324
	GAC	TCT	GCG	GTC	TAT	TTC	TGT	GCA	AGA	CGG	GGA	TCC	TAC	GGT	AGT	AAC	TAC	GAC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	D	S	A	V	Y	F	C	A	R	R	G	S	Y	G	S	N	Y	D
	333					342			351			360			369			378
	TGG	TAC	TTC	GAT	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGT
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	W	Y	F	D	V	W	G	Q	G	T	T	V	T	V	S	S	G	G
	387					396			405			414			423			432
	GGT	GGT	TCT	GGC	GGC	GGC	GGC	TCC	GGT	GGT	GGT	GGT	TCT	GAG	CTC	GTG	ATG	ACC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	G	G	S	G	G	G	G	S	G	G	G	G	S	E	L	V	M	T
	441					450			459			468			477			486
	CAG	ACT	CCA	CTC	TCC	CTG	CCT	GTC	AGT	CTT	GGA	GAT	CAA	GCC	TCC	ATC	TCT	TGC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	Q	T	P	L	S	L	P	V	S	L	G	D	Q	A	S	I	S	C
	495					504			513			522			531			540
	AGA	TCT	AGT	CAG	AGC	CTT	GTA	CAC	AGT	AAT	GGA	AAC	ACC	TAT	TTA	CAT	TGG	TAC
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	R	S	S	Q	S	L	V	H	S	N	G	N	T	Y	L	H	W	Y
	549					558			567			576			585			594
	CTG	CAG	AAG	CCA	GGC	CAG	TCT	CCA	AAG	CTC	CTG	ATC	TAC	AAA	GGT	TCC	AAC	CGA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	L	Q	K	P	G	Q	S	P	K	L	L	I	Y	K	V	S	N	R
	603					612			621			630			639			648
	TTT	TCT	GGG	GTC	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGA	TCA	GGG	ACA	GAT	TTC	ACA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	F	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T
	657					666			675			684			693			702
	CTC	AAG	ATC	AGC	AGA	GTG	GAG	GCT	GAG	GAT	CTG	GGA	GTT	TAT	TTC	TGC	TCT	CAA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	L	K	I	S	R	V	E	A	E	D	L	G	V	Y	F	C	S	Q
	711					720			729			738			747			
	AGT	ACA	CAT	GAT	GGT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTT	GAG	ATC	AAA
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3'
	S	T	H	V	P	Y	T	F	G	G	G	T	K	L	E	I	K	

Figure 6.5

24/40

	9	18	27	36	45	54
5'	GAG GTG CAG CTG CTC GAG CAG TCT GGA GCT GCG CTG GTA AGG CCT GGG ACT TCA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	E V Q L L E Q S G A A L V R P G T S					
	63 72 81 90 99 108					
	G TG AAG ATA TCC TGC AAG GCT TCT GGA TAC GCC TTC ACT AAC TAC TGG CTA GGT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	V K I S C K A S G Y A F T N Y W L G					
	117 126 135 144 153 162					
	TGG GTA AAG CAG AGG CCT GGA CAT GGA CTT GAG TGG ATT GGA GAT ATT TAC CCT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	W V K Q R P G H G L E W I G D I Y P					
	171 180 189 198 207 216					
	GGA AGT GGT AAT ACT CAC TAC AAT GAG AGG TTC AGG GGC AAA GCC ACA CTG ACT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G S G N T H Y N E R F R G K A T L T					
	225 234 243 252 261 270					
	GCA GAC AAA TCC TCG AGC ACA GCC TTT ATG CAG CTC AGT AGC CTG ACA TCT GAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	A D K S S S T A F M Q L S S L T S E					
	279 288 297 306 315 324					
	GAC TCT GCT GTC TAT TTC TGT GCA AGA TTG AGG AAC TGG GAC GAG CCT ATG GAC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	D S A V Y F C A R L R N W D E P M D					
	333 342 351 360 369 378					
	TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GGT GGT GGT TCT GGC					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	Y W G Q G T T V T V S S G G G G S G					
	387 396 405 414 423 432					
	GGC GGC GGC TCC GGT GGT GGT TCT GAG CTC CAG ATG ACC CAG TCT CCA TCT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G G G S G G G S E L Q M T Q S P S					
	441 450 459 468 477 486					
	TAT CTT GCT GCA TCT CCT GGA GAA ACC ATT ACT ATT AAT TGC AGG GCA AGT AAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	Y L A A S P G E T I T I N C R A S K					
	495 504 513 522 531 540					
	AGC ATT AGC AAA TAT TTA GCC TGG TAT CAA GAG AAA CCT GGG AAA ACT AAT AAG					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	S I S K Y L A W Y Q E K P G K T N K					
	549 558 567 576 585 594					
	CTT CTT ATC TAC TCT GGA TCC ACT TTG CAA TCT GGA ATT CCA TCA AGG TTC AGT					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	L L I Y S G S T L Q S G I P S R F S					
	603 612 621 630 639 648					
	GGC AGT GGA TCT GGT ACA GAT TTC ACT CTC ACC ATC AGT AGC CTG GAG CCT GAA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G S G S G T D F T L T I S S L E P E					
	657 666 675 684 693 702					
	GAT TTT GCA ATG TAT TAC TGT CAA CAG CAT AAT GAA TAC CCG TAC ACG TTC GGA					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	D F A M Y Y C Q Q H N E Y P Y T F G					
	711 720					
	GGG GGG ACC AAG CTT GAG ATC AAA 3'					
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
	G G T K L E I K					

Figure 6.6

25/40

	9	18	27	36	45	54
5'	GAG GTG CAG CTG CTC GAG CAG TCT GGA CCT GAG CTG GTA AGG CCT GGG ACT TCA					
	E V Q L L E Q S G A E L V R P G T S					
	63 72 81 90 99 108					
	GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC GCC TTC ACT AAC TAC TGG CTA GGT					
	V K I S C K A S G Y A F T N Y W L G					
	117 126 135 144 153 162					
	TGG GTT AAG CAG AGG CCT GGA CAT GGA CTT GAA TGG GTT GGA GAT ATT TTC CCT					
	W V K Q R P G H G L E W V G D I F P					
	171 180 189 198 207 216					
	GGA AGT GGT AAT GCT CAC TAC AAT GAG AAG TTC AAG GGC AAA GCC ACA CTG ACT					
	G S G N A H Y N E K F K G K A T L T					
	225 234 243 252 261 270					
	GCA GAC AAG TCC TCG TAC ACA GCC TAT ATG CAG CTC AGT AGC CTG ACA TCT GAG					
	A D K S S Y T A Y M Q L S S L T S E					
	279 288 297 306 315 324					
	GAC TCT GCT GTC TAT TTC TGT GCA AGA TTG CGG AAC TGG GAC GAG GCT ATG GAC					
	D S A V Y F C A R L R N W D E A M D					
	333 342 351 360 369 378					
	TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GGT GGT GGT TCT GGC					
	Y W G Q G T T V T V S S G G G S G					
	387 396 405 414 423 432					
	GGC GGC TCC GGT GGT GGT TCT GAG CTC GTG ATG ACA CAG TCT CCA TCC					
	G G G S G G G S E L V M T Q S P S					
	441 450 459 468 477 486					
	TCC CTG AGT GTG TCA GCA GGA GAG AAG GTC ACT ATG AGC TGC AAG TCC AGT CAG					
	S L S V S A G E K V T M S C K S S Q					
	495 504 513 522 531 540					
	AGT CTG TTA AAC AGT GGA AAT CAA AAG AAC TAC TTG GCC TGG TAC CAG CAG AAA					
	S L L N S G N Q K N Y L A W Y Q Q K					
	549 558 567 576 585 594					
	CCA GGG CAG CCT CCT AAA CTG TTG ATC TAC GGG GCA TCC ACT AGG GAA TCT GGG					
	P G Q P P K L L I Y G A S T R E S G					
	603 612 621 630 639 648					
	GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGA ACA GAT TTC ACT CTC ACC ATC					
	V P D R F T G S G S G T D F T L T I					
	657 666 675 684 693 702					
	AGC AGT GTG CAG GCT GAA GAC CTG GCA GTT TAT TAC TGT CAG AAT GAT TAT AGT					
	S S V Q A E D L A V Y Y C Q N D Y S					
	711 720 729 738					
	TAT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTT GAG ATC AAA -3'					
	Y P Y T F G G T K L E I K					

Figure 6.7

26 / 40

9 18 27 36 45 54
 GAG GTG CAG CTG CTC GAG CAG TCT GGA GCT GAG CTG GTG AGG CCT GGG GCT TCA
 E V Q L L E Q S G A E L V R P G A S
 63 72 81 90 99 108
 GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC GCC TTC AAT AAC TAC TGG CTA GGT
 V K I S C K A S G Y A F N N Y W L G
 117 126 135 144 153 162
 TGG GTA AAG CAG AGG CCT GGA CAT GGA CTT GAG TGG ATT GGA GAC ATT TAC CCT
 W V K Q R P G H G L E W I G D I Y P
 171 180 189 198 207 215
 GGA AGT GGA AAT ACT CAC TAC AAT GAG AGG TTC AGG GGC AAA GCC ACA CTG ACT
 G S G N T H Y N E R F R G K A T L T
 225 234 243 252 261 270
 GCA GAC AAA TCC TCG AGC ACA GCC TTT ATG CAG TTA AGT AGC CTG ACA TCT GAG
 A D K S S T A F M Q L S S L T S E
 279 288 297 306 315 324
 GAC TCT GCT GTC TAT TTC TGT GCA AGA TTG AGG AAC TGG GAC GAG GCT ATG GAC
 D S A V Y F C A R L R N W D E A M D
 333 342 351 360 369 378
 TAC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GGT GGT GGT TCT GGC
 Y W G Q G T T V T V S S G G G S G
 387 396 405 414 423 432
 GGC GGC GGC TCC GGT GGT GGT GGT TCT GAG CTC GTC ATG ACC CAG TCT CCA TCT
 G G G S G . G G S E L V M T Q S P S
 441 450 459 468 477 486
 TAT CTT GCT GCA TCT CCT GGA GAA ACC ATT ACT ATT AAT TGC AGG GCA AGT AAG
 Y L A A S P G E T I T I N C R A S K
 495 504 513 522 531 540
 AGC ATT AGC AAA TAT TTA GCC TGG TAT CAA GAG AAA CCT GGG AAA ACT AAT AAG
 S I S K Y L A W Y Q E K P G K T N K
 549 558 567 576 585 594
 CTT CTT ATC TAC TCT GGA TCC ACT TTG CAA TCT GGA ATT CCA TCA AGG TTC AGT
 L L I Y S G S T L Q S G I P S R F S
 603 612 621 630 639 648
 GGC AGT GGA TCT GGT ACA GAT TTC ACT CTC ACC ATC AGT AGC CTG GAG CCT GAA
 G S G S G T D F T L T I S S L E P E
 657 666 675 684 693 702
 GAT TTT GCA ATG TAT TAC TGT CAA CAG CAT AAT GAA TAC CCG TAC ACG TTC GGA
 D F A M Y Y C Q Q H N E Y P Y T F G
 711 720 720 720 720 720
 GGG GGG ACC AAG CTT GAG ATC AAA 3'
 G G T K L E I K

Figure 6.8

27/40

	9	18	27	36	45	54
5'	GAG GTG CAG CTG CTC GAG CAG TCT	GGA GCT GAG CTG GCG AGG CCT GGG GCT TCA				
	E V Q L L E Q S G A E L A R P G A S					
	63 72 81 90 99 108					
	GTG AAG CTG TCC TGC AAG GCT TCT GGC TAC ACC TTC ACA AAC TAT GGT TTA AGC					
	V K L S C K A S G Y T F T N Y G L S					
	117 126 135 144 153 162					
	TGG GTG AAG CAG AGG CCT GGA CAG GTC CTT GAG TGG ATT GGA GAG GTT TAT CCT					
	W V K Q R P G Q V L E W I G E V Y P					
	171 180 189 198 207 216					
	AGA ATT GGT AAT GCT TAC TAC AAT GAG AAG TTC AAG GGC AAG GCC ACA CTG ACT					
	R I G N A Y Y N E K F K G K A T L T					
	225 234 243 252 261 270					
	GCA GAC AAA TCC TCC AGC ACA GCG TCC ATG GAG CTC CGC AGC CTG ACC TCT GAG					
	A D K S S S T A S M E L R S L T S E					
	279 288 297 306 315 324					
	GAC TCT GCG GTC TAT TTC TGT GCA AGA CGG GGA TCC TAC GAT ACT AAC TAC GAC					
	D S A V Y F C A R R G S Y D T N Y D					
	333 342 351 360 369 378					
	TGG TAC TTC GAT GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GGT					
	W Y F D V W G Q G T T V T V S S G G					
	387 396 405 414 423 432					
	GGT GGT TCT GGC GGC GGC TCC GGT GGT GGT TCT GAG CTC GTG ATG ACC					
	G G S G G G S G G G G S E L V M T					
	441 450 459 468 477 486					
	CAG ACT CCA CTC TCC CTG CCT GTC AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC					
	Q T P L S L P V S L G D Q A S I S C					
	495 504 513 522 531 540					
	AGA TCT AGT CAG AGC CTT GTA CAC AGT AAT GGA AAC ACC TAT TTA CAT TGG TAC					
	R S S Q S L V H S N G N T Y L H W Y					
	549 558 567 576 585 594					
	CTG CAG AAG CCA GGC CAG TCT CCA AAG CTC CTG ATC TAC AAA GTT TCC AAC CGA					
	L Q K P G Q S P K L L I Y K V S N R					
	603 612 621 630 639 648					
	TTT TCT GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA GAT TTC ACA					
	F S G V P D R F S G S G S G T D F T					
	657 666 675 684 693 702					
	CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TTC TGC TCT CAA					
	L K I S R V E A E D L G V Y F C S Q					
	711 720 729 738 747					
	AGT ACA CAT GTT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTT GAG ATC AAA 3'					
	S T H V P Y T F G G G T K L E I K					

Figure 6.9

28 / 40

Figure 6.10

29 / 40

	9	18	27	36	45	54													
5'	GAG	GTG	CAG	CTG	CTC	GAG	CAG	TCT	GGA	GCT	GAG	CTG	GTA	AGG	CCT	GGG	ACT	TCA	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	E	V	Q	L	L	E	Q	S	G	A	E	L	V	R	P	G	T	S	
	63					72			81			90			99			108	
	GTG	AAG	ATA	TCC	TGC	AAG	GCT	TCT	GGA	TAC	GCC	TTC	ACT	AAC	TAC	TGG	CTA	GGT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	V	K	I	S	C	K	A	'S	G	Y	A	F	T	N	Y	W	L	G	
	117					126			135			144			153			162	
	TGG	GTA	AAG	CAG	AGG	CCT	GGA	CAT	GGA	CTT	GAG	TGG	ATT	GGA	GAT	ATT	TTC	CCT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	W	V	K	Q	R	P	G	H	G	L	E	W	I	G	D	I	F	P	
	171					180			189			198			207			216	
	GGA	AGT	GGT	AAT	ATC	CAC	TAC	AAT	GAG	AAG	TTC	AAG	GGC	AAA	GCC	ACA	CTG	ACT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	G	S	G	N	I	H	Y	N	E	K	F	K	G	K	A	T	L	T	
	225					234			243			252			261			270	
	GCA	GAC	AAA	TCT	TCG	AGC	ACA	GCC	TAT	ATG	CAG	CTC	AGT	AGC	CTG	ACA	TTT	GAG	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	A	D	K	S	S	S	T	A	Y	M	Q	L	S	S	L	T	F	E	
	279					288			297			306			315			324	
	GAC	TCT	GCT	GTC	TAT	TTC	TGT	GCA	AGA	CTG	AGG	AAC	TGG	GAC	GAG	CCT	ATG	GAC	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	D	S	A	V	Y	F	C	A	R	L	R	N	W	D	E	P	M	D	
	333					342			351			360			369			378	
	TAC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGT	GGT	TCT	GGC		
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	Y	W	G	Q	G	T	T	V	T	V	S	S	G	G	G	G	S	G	
	387					396			405			414			423			432	
	GGC	GGC	GGC	TCC	GGT	GGT	GGT	TCT	GAG	CTC	GTG	ATG	ACA	CAG	TCT	CCA	TCC		
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	G	G	G	S	G	G	G	S	E	L	V	M	T	Q	S	P	S		
	441					450			459			468			477			486	
	TCC	CTG	ACT	GTG	ACA	GCA	GGA	GAG	AAG	GTC	ACT	ATG	AGC	TGC	AAG	TCC	AGT	CAG	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	S	L	T	V	T	A	G	E	K	V	T	M	S	C	K	S	S	Q	
	495					504			513			522			531			540	
	AGT	CTG	TTA	AAC	AGT	GGA	AAT	CAA	AAG	AAC	TAC	TTG	ACC	TGG	TAC	CAG	CAG	AAA	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	S	L	L	N	S	G	N	Q	K	N	Y	L	T	W	Y	Q	Q	K	
	549					558			567			576			585			594	
	CCA	GGG	CAG	CCT	CCT	AAA	CTG	TTG	ATC	TAC	TGG	GCA	TCC	ACT	AGG	GAA	TCT	GGG	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	P	G	Q	P	P	K	L	L	I	Y	W	A	S	T	R	E	S	G	
	603					612			621			630			639			648	
	GTC	CCT	GAT	CGC	TTC	ACA	GGC	AGT	GGA	TCT	GGA	ACA	GAT	TTC	ACT	CTC	ACC	ATC	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T	I	
	657					666			675			684			693			702	
	ACC	AGT	GTG	CAG	GCT	GAA	GAC	CTG	GCA	GTT	TAT	TAC	TGT	CAG	AAT	GAT	TAT	AGT	
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	S	S	V	Q	A	E	D	L	A	V	Y	Y	C	Q	N	D	Y	S	
	711					720			729			738							
	TAT	CCG	CTG	ACG	TTC	GGT	GCT	GGG	ACC	AAG	CTT	GAG	ATC	AAA	3'				
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	Y	P	L	T	F	G	A	G	T	K	L	E	I	K					

Figure 7

30 / 40

	9	18	27	36	45	54											
5'	GAG GTG CAG CTG CTC GAG CAG TCT GGA GCT GAG CTG GTA AGG CCT GGG ACT TCA																
	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -											
E	V	Q	L	L	E	Q	S	G	A	E	L	V	R	P	G	T	S
63					72			81			90			99			108
GTG	AAG	ATA	TCC	TGC	AAG	GCT	TCT	GGA	TAC	GCC	TTC	ACT	AAC	TAC	TGG	CTA	GGT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
V	K	I	S	C	K	A	S	G	Y	A	F	T	N	Y	W	L	G
117					126			135			144			153			162
TGG	GTT	AAG	CAG	AGG	CCT	GGA	CAT	GGA	CTT	GAA	TGG	GTT	GGA	GAT	ATT	TTC	CCT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
W	V	K	Q	R	P	G	H	G	L	E	W	V	G	D	I	F	P
171					180			189			198			207			216
GGA	AGT	GGT	AAT	GCT	CAC	TAC	AAT	GAG	AAG	TTC	AAG	GGC	AAA	GCC	ACA	CTG	ACT
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
G	S	G	N	A	H	Y	N	E	K	F	K	G	K	A	T	L	T
225					234			243			252			261			270
GCA	GAC	AAG	TCC	TCG	TAC	ACA	GCC	TAT	ATG	CAG	CTC	AGT	AGC	CTG	ACA	TCT	GAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
A	D	K	S	S	Y	T	A	Y	M	Q	L	S	S	L	T	S	E
279					288			297			306			315			324
GAC	TCT	GCT	GTC	TAT	TTC	TGT	GCA	AGA	TTG	CGG	AAC	TGG	GAC	GAG	GCT	ATG	GAC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
D	S	A	V	Y	F	C	A	R	L	R	N	W	D	E	A	M	D
333					342			351			360			369			378
TAC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GGT	GGT	GGT	TCT	GGC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
Y	W	G	Q	G	T	T	V	T	V	S	S	G	G	G	G	S	G
387					396			405			414			423			432
GGC	GGC	GGC	TCC	GGT	GGT	GGT	GGT	TCT	GAG	CTC	GTG	ATG	ACA	CAG	TCT	CCA	TCC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
G	G	G	S	G	G	G	S	E	L	V	M	T	Q	S	P	S	
441					450			459			468			477			486
TCC	CTG	GCT	ATG	TCA	GTA	GGA	CAG	AAG	GTC	ACT	ATG	AGC	TGC	AAG	TCC	AGT	CAG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
S	L	A	M	S	V	G	Q	K	V	T	M	S	C	K	S	S	Q
495					504			513			522			531			540
AGC	CTT	TTA	AAT	AGT	AGC	AAT	CAA	AAG	AAC	TAT	TTG	GCC	TGG	TAC	CAG	CAG	AAA
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
S	L	N	S	S	N	Q	K	N	Y	L	A	W	Y	Q	Q	K	
549					558			567			576			585			594
CAA	GGG	CAG	CCT	CCT	AAA	CTG	CTT	ATC	TAT	GGG	GCA	TCC	ATT	AGA	GAA	TCT	TGG
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
Q	G	Q	P	P	K	L	L	I	Y	G	A	S	I	R	E	S	W
603					612			621			630			639			648
GTC	CCT	GAT	CGA	TTC	ACA	GGA	AGT	GGA	TCT	GGG	ACA	GAC	TTC	ACT	CTC	ACC	ATC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
V	P	D	R	F	T	G	S	G	S	G	T	D	F	T	L	T	I
657					666			675			684			693			702
AGC	AGT	GTG	AAG	GCT	GAA	GAC	CTG	GCA	GTT	TAT	TAC	TGT	CAG	CAA	TAT	TAT	AGC
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
S	S	V	K	A	E	D	L	A	V	Y	Y	C	Q	Q	Y	Y	S
711					720			729			738						
TAT	CCG	TAC	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTT	GAG	ATC	AAA	3'			
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	
Y	P	Y	T	F	G	G	T	K	L	E	I	K					

Figure 8.1

ELISA -analysis
CD 80-Anti-17-1A scFv 3-1 – 5-13 (PS)
Detection: anti – CD 80

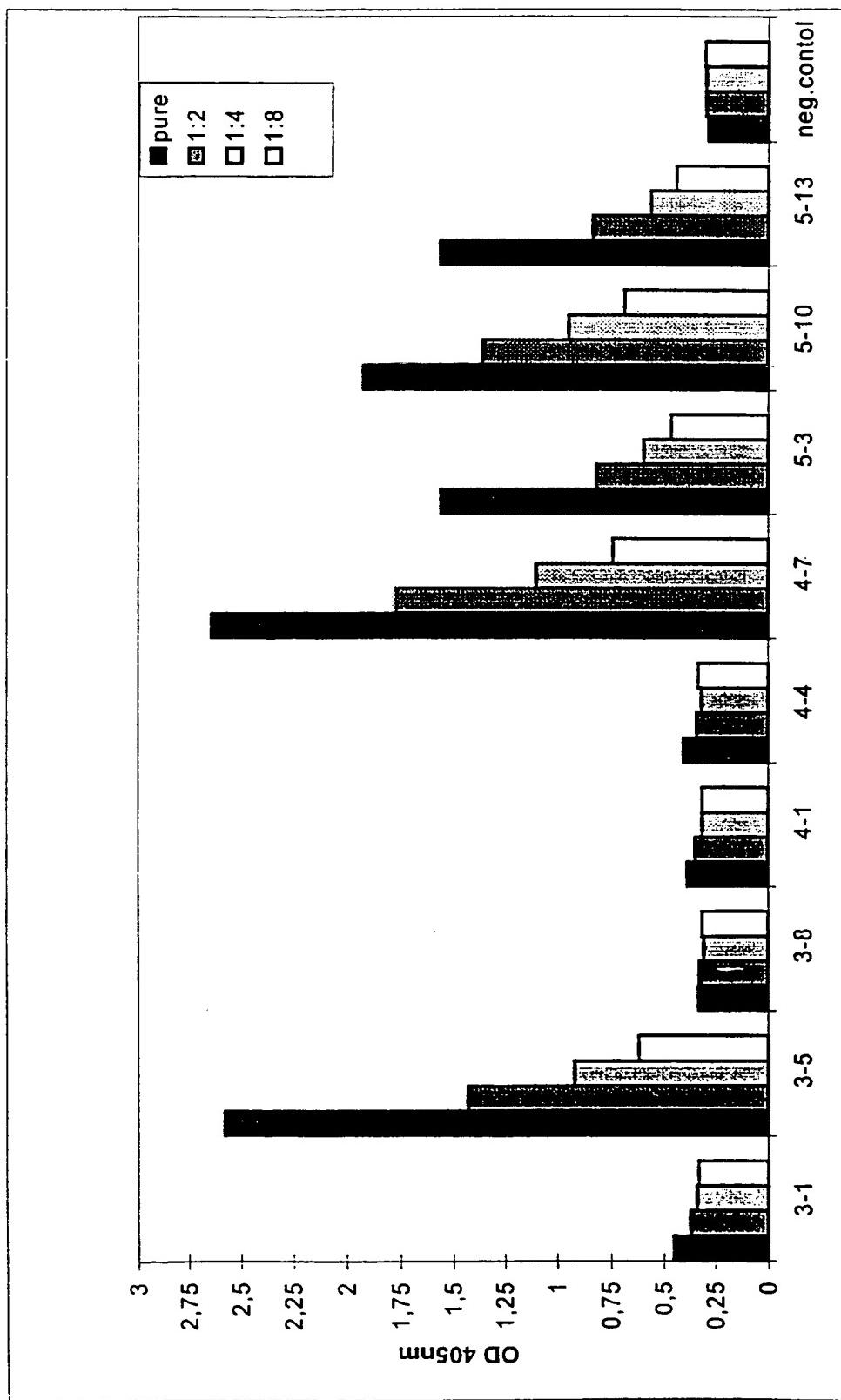


Figure 8.2

ELISA -analysis
CD 80-Anti-17-1A scFv 3-1 - 5-13 (1. Amp.)
Detection: anti - CD 80

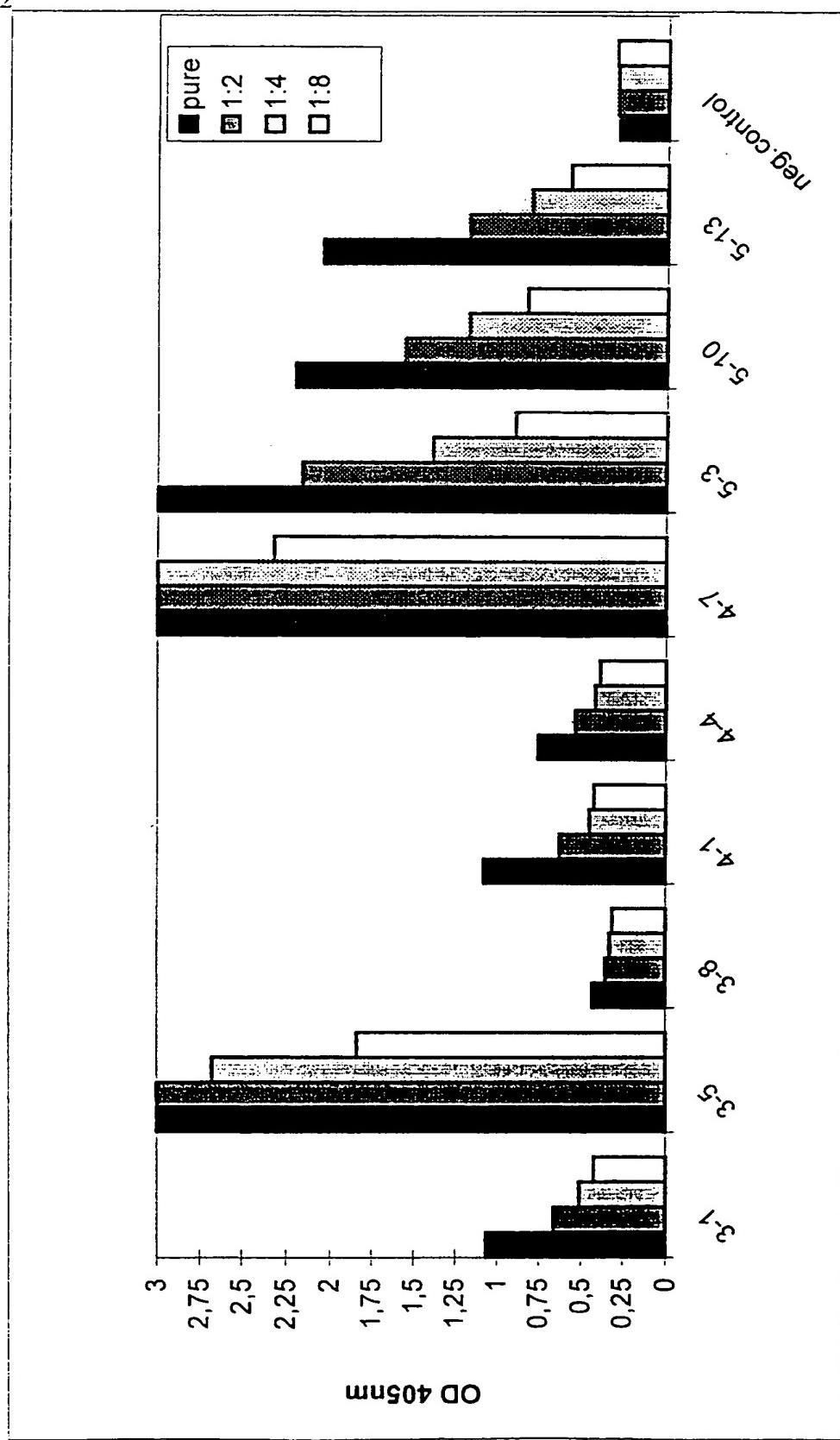


Figure 8.3

ELISA -analysis
CD 80-VD4.5V_k8 scFv (PS) and CD 80-Mach scFv (PS)
Detection: anti - CD 80

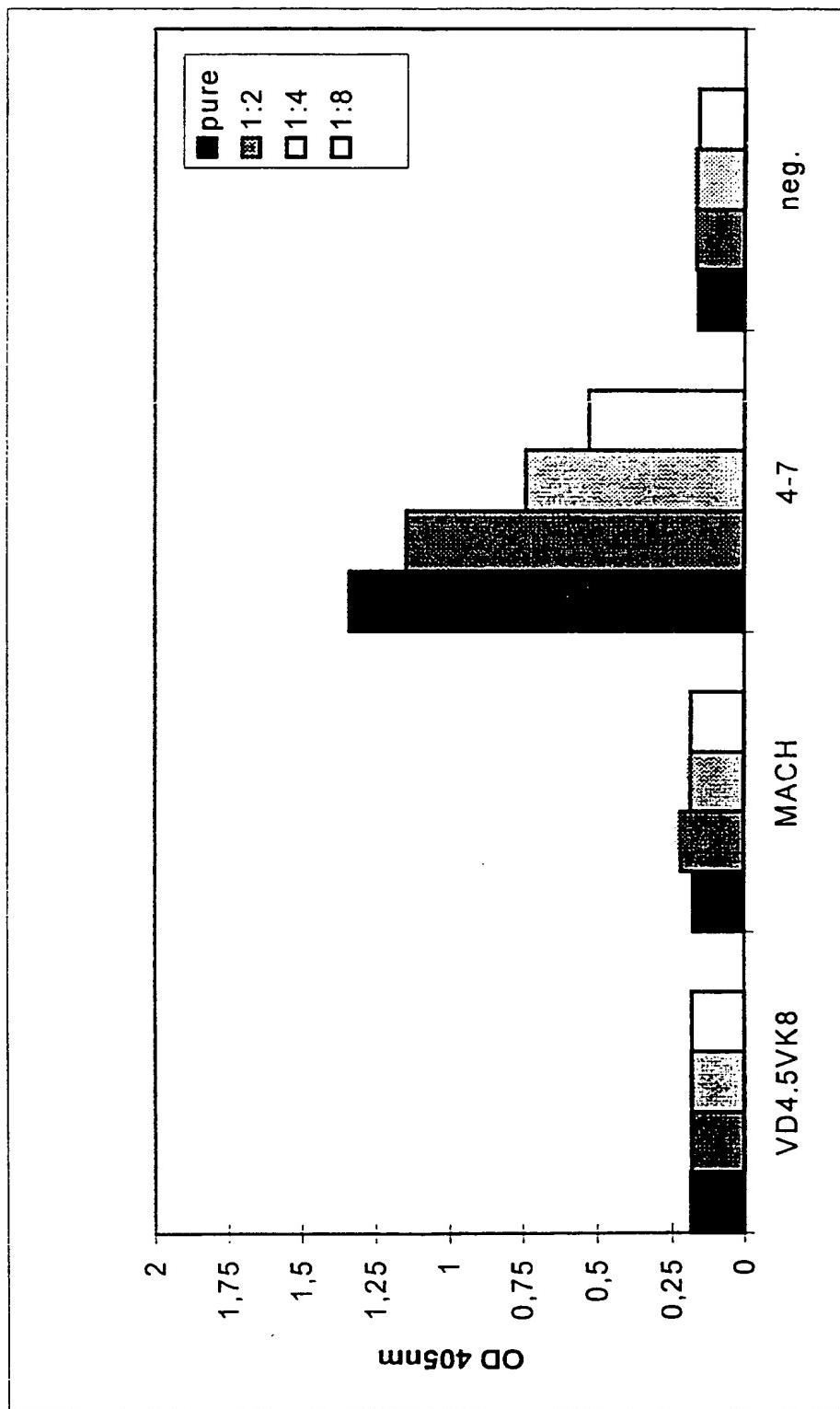


Figure 8.4

ELISA -analysis
CD 80-VD4.5V_k8 scFv (1. Amp.) and CD 80-Mach scFv (1. Amp.)
Detection: anti - CD 80

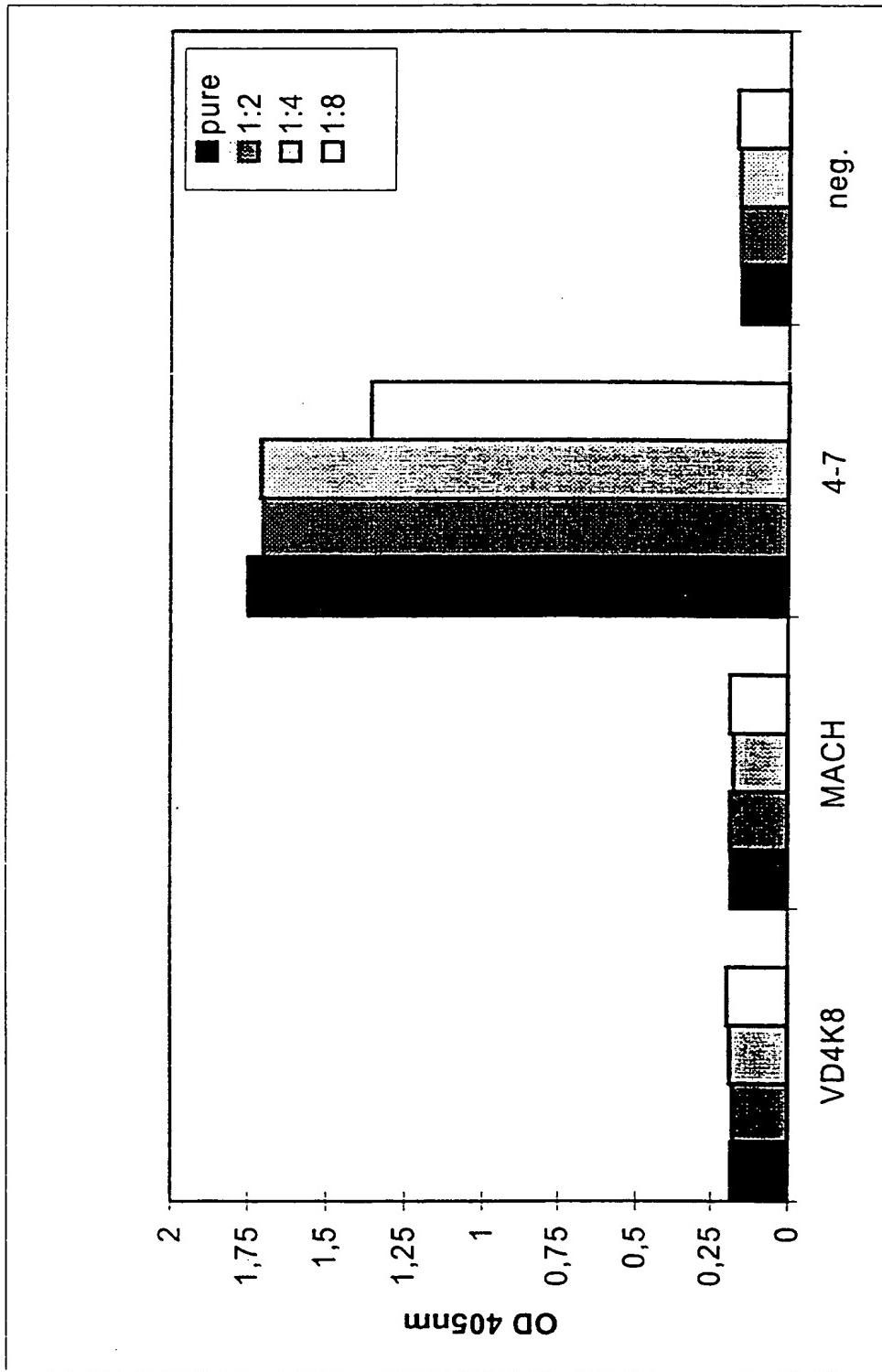


Figure 9.1

Part 1

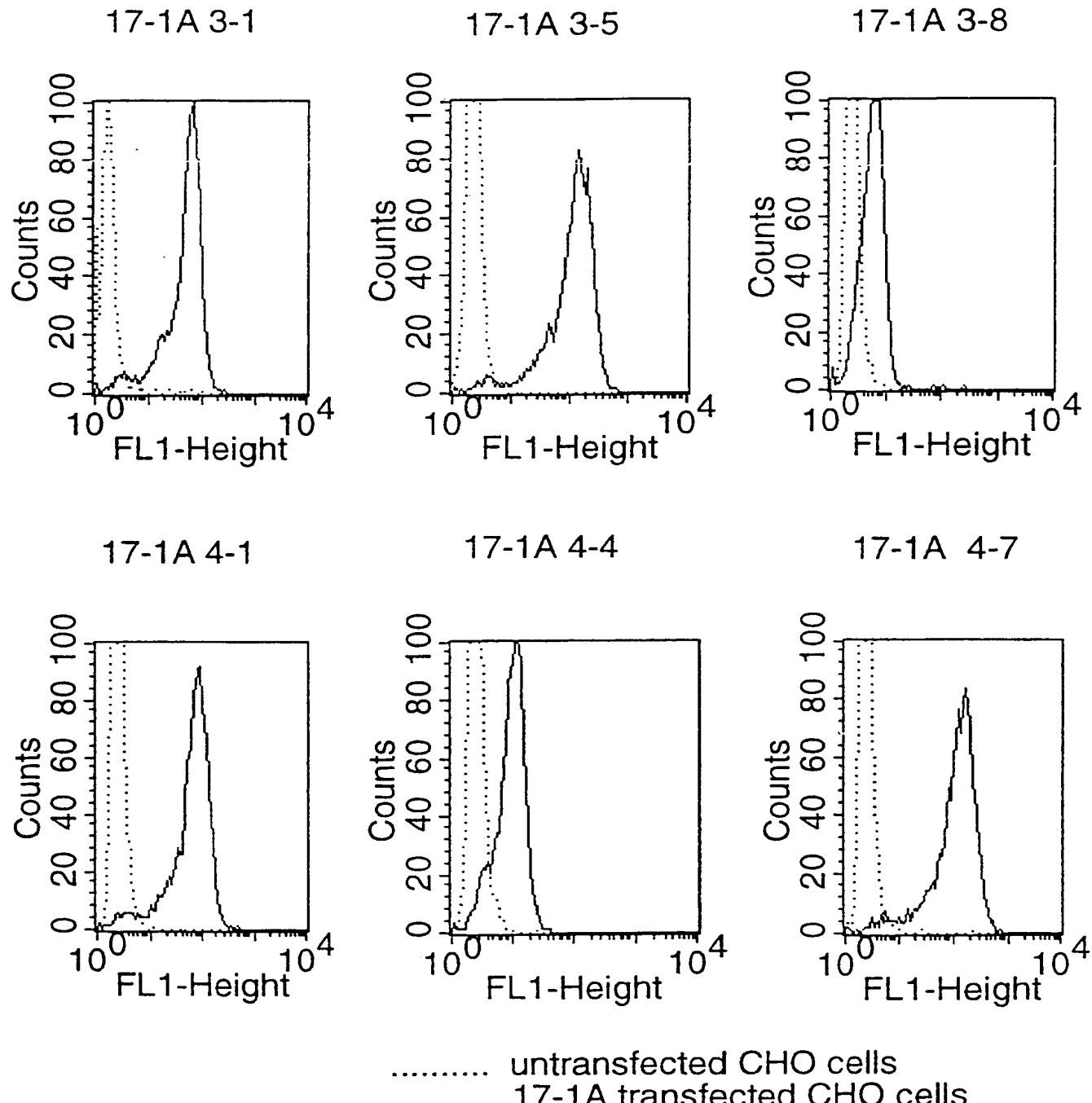


Figure 9.1

Part 2

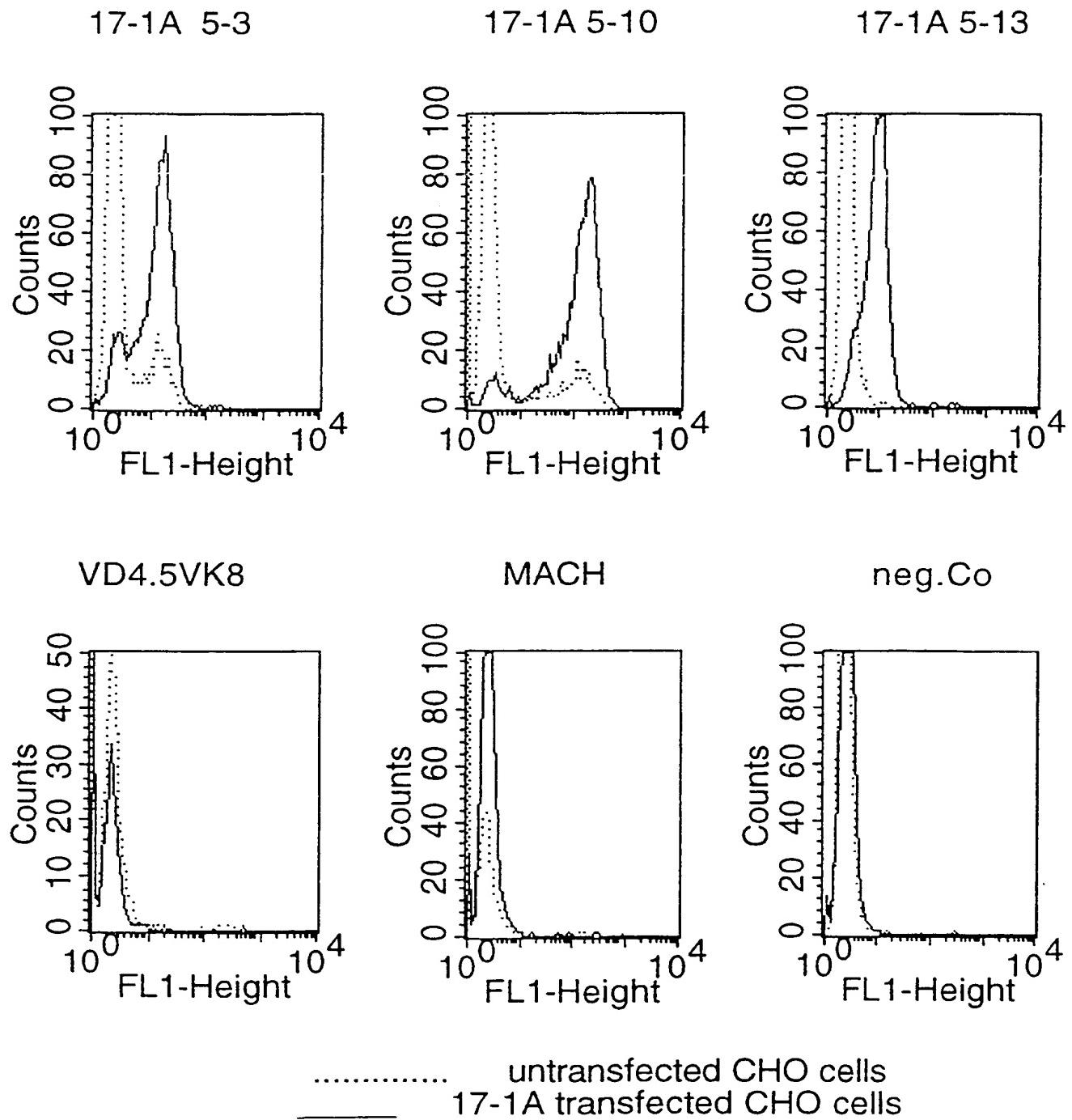


Figure 9.2

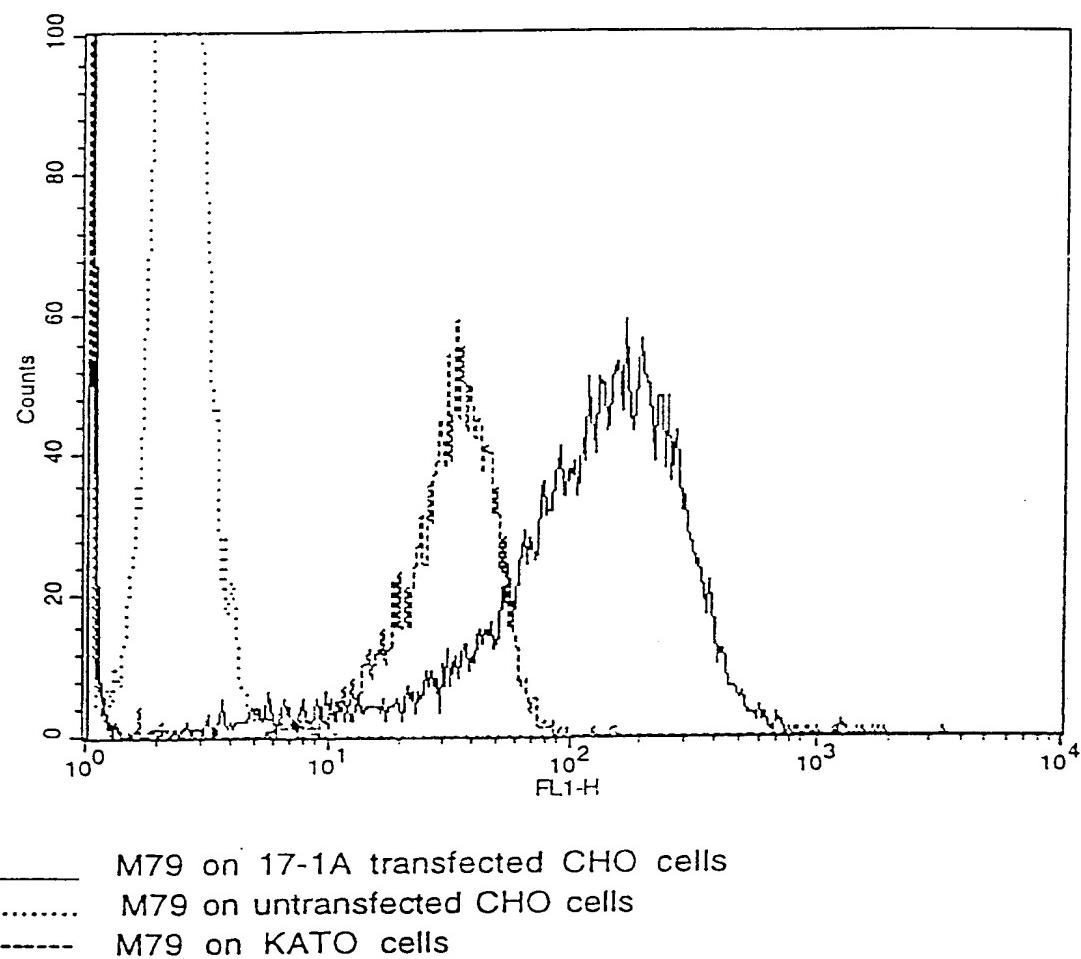
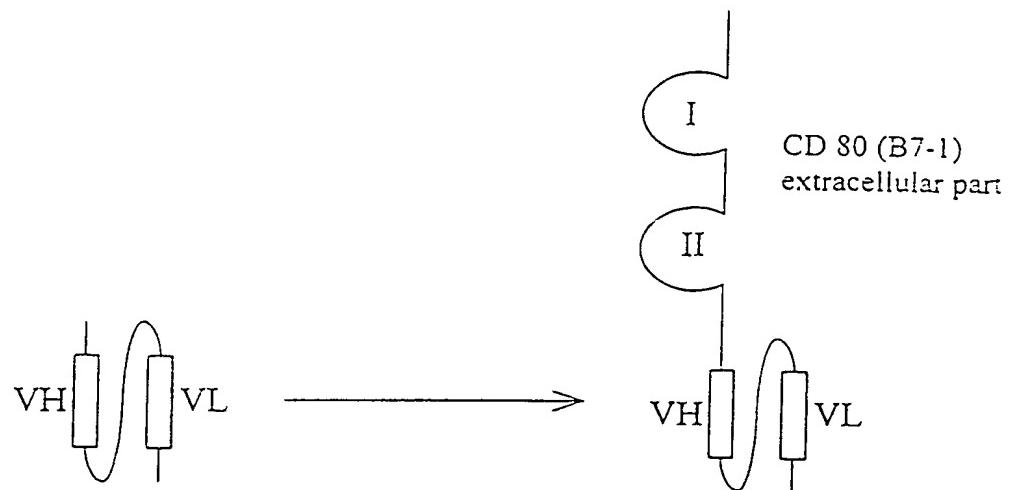


Figure 10

1) The Conventional approach

Randomly selected antigen-specific VH/VL-pairs that bind to their antigen as free or N-terminally located scFv-fragments or as whole antibody molecules

Frequent loss of antigen binding after fusion of another protein domain to the N-terminus of the scFv-fragment



2) The method of invention

VH/VL-pairs selected by the method of the invention

High frequency of antigen binding after fusion of another protein domain to the N-terminus of the scFv-fragment

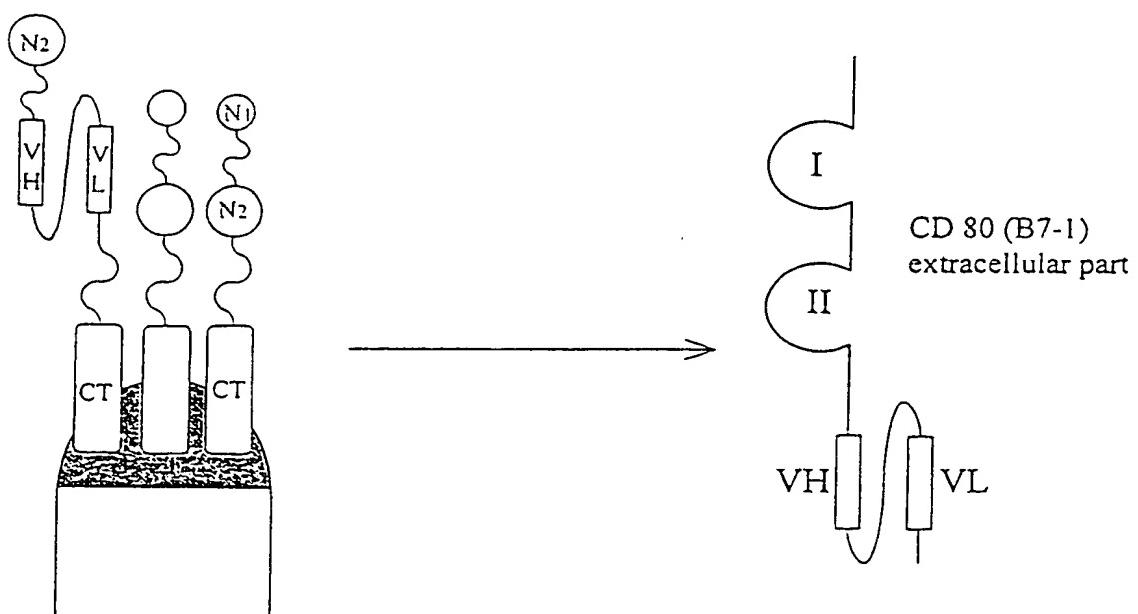


Figure 11

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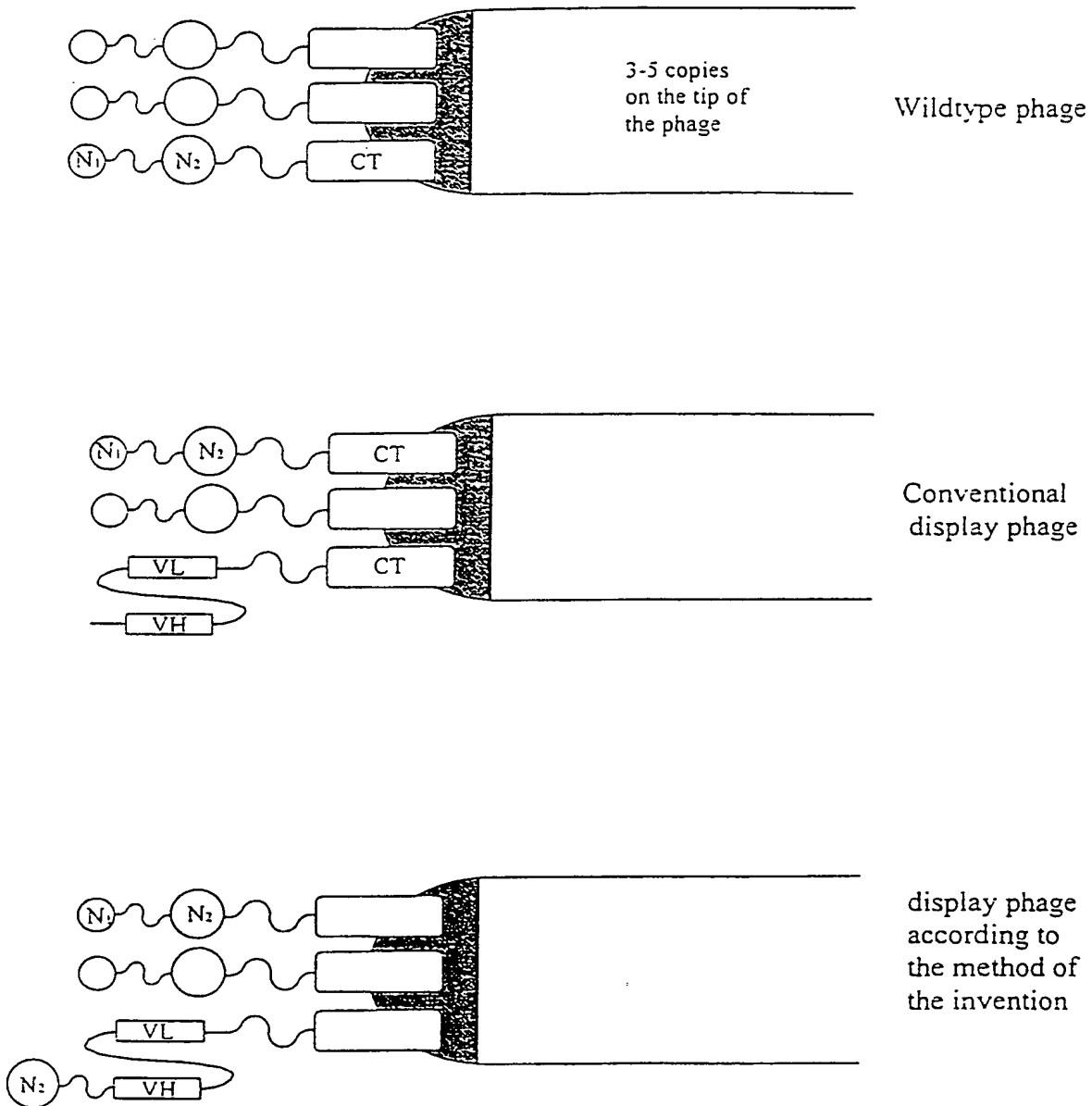


Figure 12

ELISA on different anti 17-1A-CD54, anti 17-1A CD58, anti 17-1A

CD86 constructs

